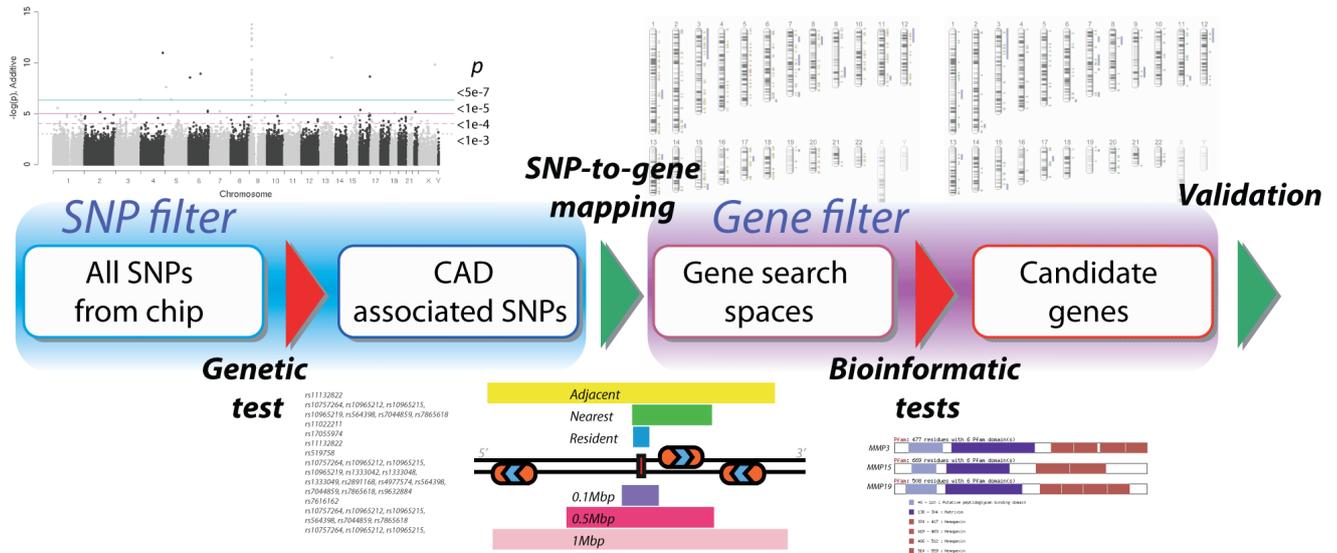


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Supp. Figure S1. Workflow diagram. SNPs are filtered for significance at different thresholds. These SNPs are then naïvely clustered if in close proximity (within 50Kbp). SNP loci are then mapped to genes in 1 of 6 ways, creating 6 gene search space sets for each significance threshold. Each gene search space is then used as input into *Gentrepid*, with bioinformatic tests performed, resulting in a list of prioritised disease candidate genes.

Supp. Table S1. *Gentrepid* gene predictions for the CAD phenotype

Gene	Locus	Genetic support	Resident	Near	Adjacent	0.1Mbp	0.5Mbp	1Mbp	Method	Common biological support	Score	Rank
<i>ENO1</i>	1p36.23	●			✓	✓	✓		CPS-s	Metabolic pathways	0000	1
<i>RERE</i>	1p36.23	●				✓	✓		PPI-ab	11143, 6613, 2202, 10346, 7994	0	48
<i>H6PD</i>	1p36.22	●			✓	✓	✓		CPS-s	Metabolic pathways	0000	1
<i>OPRD1</i>	1p35.3	●			✓	✓	✓	✓	CMP-ab	7TM_GPCR_Srx 7TM_GPCR_Srv 7TM_GPCR_Srx 7TM_GPCR_Srv 7tm_1	00000	8
<i>RAB42</i>	1p35.3	●						✓	CMP-ab	Arf Miro Ras	00000	55
<i>EPB41</i>	1p35.3	●		✓	✓	✓	✓	✓	CMP-ab	FA FERM_C FERM_M FERM_N	00000	1
<i>PTPRU</i>	1p35.3	●						✓	CMP-ab	MAM Y_phosphatase fn3	00000	66
<i>MECR</i>	1p35.3	●						✓	CPS-s	Metabolic pathways	0000	1
<i>CSMD2</i>	1p34.3	●●●	✓	✓	✓	✓	✓	✓	CMP-ab	CUB Sushi	00000	1
<i>DOCK7</i>	1p31.3	●			✓	✓	✓	✓	CMP-ab	DUF3398 Ded_cyto	00000	29
<i>PTGFR</i>	1p31.1	●						✓	CMP-ab	7TM_GPCR_Srv 7TM_GPCR_Srx 7tm_1	00000	57
<i>NEGR1</i>	1p31.1	●			✓				CMP-ab	I-sset V-set ig	00000	28
<i>FPGT</i>	1p31.1	●				✓	✓	✓	CPS-s	Metabolic pathways	0000	1
<i>HFM1</i>	1p22.2	●			✓	✓	✓	✓	CMP-ab	DEAD Helicase_C ResIII	00000	21
<i>CDC7</i>	1p22.2	●			✓	✓	✓		PPI-ab	5001, 1017, 10963, 4174, 1029, 1018, 84078, 56902, 51082, 5708, 84940, 5707, 51719	0	59
<i>COL11A1</i>	1p21.1	●	✓	✓	✓	✓	✓	✓	CPS-s	ECM-receptor interaction	0	1
<i>SORT1</i>	1p13.3	●●				✓	✓	✓	CMP-ab	BNR	0000	39
<i>CELSR2</i>	1p13.3	●●	✓	✓	✓	✓	✓	✓	CMP-ab	EGF Laminin_G_1 Laminin_G_2	00000	3
<i>PSMA5</i>	1p13.3	●●					✓	✓	CMP-ab	Proteasome Proteasome_A_N	00000	6
<i>AMPD2</i>	1p13.3	●●						✓	CPS-s	Metabolic pathways	0000	1
<i>SARS</i>	1p13.3	●●				✓	✓		CPS-ab	Aminoacyl-tRNA biosynthesis	00	2
<i>GSTM4</i>	1p13.3	●●						✓	CPS-ab	Drug metabolism - cytochrome P450	00	7
<i>GSTM5</i>	1p13.3	●●						✓	CPS-ab	Drug metabolism - cytochrome P450	00	7
<i>GSTM3</i>	1p13.3	●●						✓	CPS-ab	Drug metabolism - cytochrome P450	00	7
<i>GSTM2</i>	1p13.3	●●						✓	CPS-ab	Drug metabolism - cytochrome P450	00	7
<i>GSTM1</i>	1p13.3	●●						✓	CPS-ab	Drug metabolism - cytochrome P450	00	7
<i>WDR47</i>	1p13.3	●●					✓	✓	PPI-ab	6919, 55743	0	166
<i>NRAS</i>	1p13.2	●						✓	CMP-ab	Arf GTP_EFTU Miro Ras	00000	30
<i>DENND2C</i>	1p13.2	●						✓	CMP-ab	DENN dDENN uDENN	00000	35
<i>AMPD1</i>	1p13.2	●						✓	CPS-s	Metabolic pathways	0000	1
<i>ADAM30</i>	1p12	●						✓	CMP-ab	Disintegrin Pep_M12B_propep Reprolysin	00000	52
<i>NOTCH2</i>	1p12	●						✓	CMP-ab	EGF EGF_2 EGF_CA	00000	58
<i>HSD3B1</i>	1p12	●			✓	✓	✓	✓	CPS-s	Metabolic pathways	0000	1
<i>HSD3B2</i>	1p12	●						✓	CPS-s	Metabolic pathways	0000	1
<i>PHGDH</i>	1p12	●						✓	CPS-s	Metabolic pathways	0000	1
<i>HAO2</i>	1p12	●						✓	CPS-s	Metabolic pathways	0000	1
<i>MAN1A2</i>	1p12	●						✓	CPS-s	Metabolic pathways	0000	1
<i>HMGCS2</i>	1p12	●						✓	CPS-s	Metabolic pathways	0000	1
<i>PI4KB</i>	1q21.2	●						✓	CPS-s	Metabolic pathways	0000	1
<i>RFX5</i>	1q21.2	●						✓	CPS-ab	Tuberculosis	000	5
<i>OAZ3</i>	1q21.3	●			✓	✓	✓	✓	CMP-ab	ODC_AZ	0000	39
<i>BCAN</i>	1q23.1	●						✓	CMP-ab	EGF Lectin_C Sushi V-set Xlink	00000	10
<i>INSRR</i>	1q23.1	●						✓	CMP-ab	Furin-like Pkinase Pkinase_Tyr Recep_L_domain	00000	12
<i>OR6N2</i>	1q23.1	●			✓	✓	✓	✓	CPS-ab	Olfactory transduction	000	1
<i>OR6K6</i>	1q23.1	●			✓	✓	✓	✓	CPS-ab	Olfactory transduction	000	1
<i>OR6N1</i>	1q23.1	●				✓	✓	✓	CPS-ab	Olfactory transduction	0	5
<i>OR10R2</i>	1q23.1	●						✓	CPS-ab	Olfactory transduction	0000	2
<i>OR10K1</i>	1q23.1	●						✓	CPS-ab	Olfactory transduction	0000	2
<i>OR10T2</i>	1q23.1	●						✓	CPS-ab	Olfactory transduction	0000	2
<i>OR10K2</i>	1q23.1	●						✓	CPS-ab	Olfactory transduction	0000	2
<i>OR10X1</i>	1q23.1	●						✓	CPS-ab	Olfactory transduction	0000	1
<i>OR6K2</i>	1q23.1	●						✓	CPS-ab	Olfactory transduction	0000	1
<i>OR6K3</i>	1q23.1	●						✓	CPS-ab	Olfactory transduction	0000	1
<i>OR6Y1</i>	1q23.1	●						✓	CPS-ab	Olfactory transduction	0000	1
<i>OR10Z1</i>	1q23.1	●						✓	CPS-ab	Olfactory transduction	0000	1
<i>NTRK1</i>	1q23.1	●						✓	CPS-ab	Pathways in cancer	0	9

<i>CADM3</i>	1q23.2	•					✓	CMP-ab	C1-set C2-set_2 I-sset V-set ig	ooooo	21
<i>CACNA1E</i>	1q25.3	••			✓		✓	CPS-s	Type II diabetes mellitus	◊	1
<i>PLXNA2</i>	1q32.2	••	✓	✓	✓	✓	✓	CPS-ab	Axon guidance	◊◊◊	2
<i>CAPN2</i>	1q41	••			✓		✓	CMP-ab	Calpain_III Peptidase_C2	ooooo	38
<i>CAPN8</i>	1q41	••		✓	✓	✓	✓	CMP-ab	Calpain_III Peptidase_C2	ooooo	38
<i>AIDA</i>	1q41	•			✓	✓	✓	MIR-ab	MI0000270	◊◊	1
<i>PYCR2</i>	1q42.12	•					✓	CPS-s	Metabolic pathways	◊◊◊◊	1
<i>EPHX1</i>	1q42.12	•		✓	✓	✓	✓	CPS-ab	Eicosanoid Metabolism	◊	5
<i>H3F3A</i>	1q42.12	•					✓	CPS-ab	Systemic lupus erythematosus	◊◊◊	3
<i>CAPN9</i>	1q42.2	••			✓		✓	CMP-ab	Calpain_III Peptidase_C2	ooooo	38
<i>EGLN1</i>	1q42.2	••					✓	CPS-ab	Pathways in cancer	◊	9
<i>NID1</i>	1q42.3	•					✓	CMP-s	4040 Ldl_recept_b	••	3
<i>ERO1LB</i>	1q42.3	•			✓	✓	✓	PPI-ab	8602, 5685, 55226, 10885	◊◊	316
<i>CHRM3</i>	1q43	•					✓	CMP-ab	7TM_GPCR_Srsx 7TM_GPCR_Srx 7tm_1	ooooo	65
<i>ACTN2</i>	1q43	•					✓	PPI-s	4846	◊◊	17
<i>HNRNPU</i>	1q44	•			✓		✓	PPI-s	3667	◊◊◊◊	7
<i>ADAM17</i>	2p25.1	•					✓	CMP-ab	Disintegrin Pep_M12B_propepl Reprolysin	ooooo	52
<i>LPIN1</i>	2p25.1	•					✓	CMP-ab	LNS2 Lipin_N	ooooo	68
<i>MBOAT2</i>	2p25.1	•					✓	CPS-s	Metabolic pathways	◊◊◊◊	1
<i>ASAP2</i>	2p25.1	•			✓	✓	✓	CPS-ab	ADP-sRibosylation Factor	◊◊◊	3
<i>ID2</i>	2p25.1	•			✓		✓	CPS-ab	TGF-beta signaling pathway	◊	16
<i>PNPT1</i>	2p16.1	•					✓	CMP-ab	RNase_PH RNase_PH_C	ooooo	74
<i>CTNNA2</i>	2p12	•			✓		✓	CPS-ab	Pathways in cancer	◊◊◊	2
<i>NPAS2</i>	2q11.2	•					✓	CMP-ab	HLH PAS PAS_3	ooooo	51
<i>EDAR</i>	2q13	•					✓	CPS-s	Cytokine-cytokine receptor interaction	◊◊◊	2
<i>GLI2</i>	2q14.2	•••			✓		✓	CPS-ab	Pathways in cancer	◊◊◊	2
<i>ARL5A</i>	2q23.3	•					✓	CMP-ab	Arf Gtr1_RagA Miro Ras SRPRB	ooooo	5
<i>CACNB4</i>	2q23.3	•	✓	✓	✓	✓	✓	CPS-ab	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	◊	4
<i>STAM2</i>	2q23.3	•					✓	CPS-ab	Jak-STAT signaling pathway	◊	10
<i>UPP2</i>	2q24.1	••					✓	CPS-s	Metabolic pathways	◊◊◊◊	1
<i>ABCA12</i>	2q35	•	✓	✓	✓	✓	✓	CMP-s	19 ABC_tran	•	2
<i>ATIC</i>	2q35	•			✓		✓	CPS-s	Metabolic pathways	◊◊◊◊	1
<i>BARD1</i>	2q35	•					✓	CPS-ab	BRCA1-dependent Ub-ligase activity	◊◊	6
<i>FNI</i>	2q35	•					✓	PPI-s	4018	◊◊◊◊	11
<i>IRS1</i>	2q36.3	••			✓	✓	✓	CPS-s	2q36 Insulin signaling pathway	◊	1
<i>HTR2B</i>	2q37.1	•					✓	CMP-ab	7TM_GPCR_Srsx 7TM_GPCR_Srv 7tm_1	ooooo	69
<i>RAB17</i>	2q37.3	•			✓		✓	CMP-ab	Arf Gtr1_RagA Miro Ras	ooooo	11
<i>KLHL30</i>	2q37.3	•					✓	CMP-ab	BACK BTB Kelch_1	ooooo	50
<i>CAPN10</i>	2q37.3	•			✓	✓	✓	CMP-ab	Calpain_III Peptidase_C2	ooooo	38
<i>SNED1</i>	2q37.3	•					✓	CMP-ab	EGF EGF_2 EGF_CA	ooooo	58
<i>RNPEPL1</i>	2q37.3	•	✓	✓	✓	✓	✓	CMP-ab	Peptidase_M1	oooo	17
<i>SCLY</i>	2q37.3	•					✓	CPS-s	Metabolic pathways	◊◊◊◊	1
<i>AGXT</i>	2q37.3	•					✓	CPS-s	Metabolic pathways	◊◊◊◊	1
<i>GPC1</i>	2q37.3	•					✓	PPI-ab	7422, 2885, 80781	◊	53
<i>SRGAP3</i>	3p25.3	•					✓	CMP-ab	3pter-p21, 3p21.2-p14.1 FCH RhoGAP SH3_1 SH3_2	ooooo	32
<i>VHL</i>	3p25.3	•					✓	CPS-s	Hypoxia-Inducible Factor in the Cardiovascular System	◊◊	3
<i>ARPC4</i>	3p25.3	•			✓	✓	✓	CPS-ab	Bacterial invasion of epithelial cells	◊	19
<i>FANCD2</i>	3p25.3	•					✓	CPS-ab	BRCA1-dependent Ub-ligase activity	◊◊	6
<i>CAMK1</i>	3p25.3	•			✓	✓	✓	CPS-ab	fMLP induced chemokine gene expression in HMC-1 cells	◊	15
<i>IRAK2</i>	3p25.3	•					✓	CPS-ab	Tuberculosis	◊◊◊	5
<i>OXSM</i>	3p24.2	•					✓	CPS-s	Metabolic pathways	◊◊◊◊	1
<i>CX3CR1</i>	3p22.2	••			✓		✓	CPS-s	Cytokine-cytokine receptor interaction	◊◊◊	2
<i>MLH1</i>	3p22.2	•					✓	CPS-ab	Pathways in cancer	◊	9
<i>CCR8</i>	3p22.1	••					✓	CMP-s	1524 7TM_GPCR_Srsx 7tm_1	•	6
<i>RPSA</i>	3p22.1	••			✓	✓	✓	PPI-ab	11128, 3778	◊	43
<i>CCR3</i>	3p21.31	•			✓		✓	CMP-s	1524 7TM_GPCR_Srsx 7tm_1	•	7
<i>CCR1</i>	3p21.31	•			✓		✓	CMP-s	1524 7TM_GPCR_Srsx 7tm_1	•	9
<i>EXOSC7</i>	3p21.31	•			✓		✓	CMP-ab	RNase_PH RNase_PH_C	ooooo	74
<i>CCR9</i>	3p21.31	•					✓	CPS-s	Cytokine-cytokine receptor interaction	◊◊◊	2
<i>CCR2</i>	3p21.31	•					✓	CPS-s	Cytokine-cytokine receptor interaction	◊◊◊	2
<i>CCR5</i>	3p21.31	•					✓	CPS-s	Cytokine-cytokine receptor interaction	◊◊◊	2
<i>XCR1</i>	3p21.31	•			✓		✓	CPS-s	Cytokine-cytokine receptor interaction	◊◊◊	2
<i>CXCR6</i>	3p21.31	•					✓	CPS-s	Cytokine-cytokine receptor interaction	◊◊◊	2

<i>LARS2</i>	3p21.31	●			✓	✓	✓	✓	CPS-ab	Valine, leucine and isoleucine biosynthesis	0	3
<i>SACMIL</i>	3p21.31	●							PPI-ab	10564	000	98
<i>FYCO1</i>	3p21.31	●						✓	PPI-ab	26227, 3861, 506, 2023, 3320, 3326, 3868, 3860, 1832, 6950, 3187, 4174, 5984, 3857, 47, 4637, 6155, 6632, 6229, 6160, 5478, 2969, 3192, 6128, 708, 5708, 5790, 9859, 54800, 25902, 22879, 10808, 81631, 51493	0	31
<i>IL17RB</i>	3p21.1	●							CPS-s	Cytokine-cytokine receptor interaction	000	2
<i>CACNA1D</i>	3p21.1	●							CPS-s	Type II diabetes mellitus	00	4
<i>CACNA2D3</i>	3p14.3	●	✓	✓	✓	✓	✓	✓	CPS-ab	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	0	4
<i>FHIT</i>	3p14.2	●	✓	✓	✓	✓	✓	✓	CPS-ab	Small cell lung cancer	000	4
<i>GBE1</i>	3p12.2	●	✓	✓	✓	✓	✓	✓	CPS-s	Metabolic pathways	0000	1
<i>CADM2</i>	3p12.1	●							CMP-ab	C2-set_2 I-sset V-set ig	00000	17
<i>B4GALT4</i>	3q13.32	●							CPS-s	Metabolic pathways	0000	1
<i>CD86</i>	3q13.33	●							CPS-ab	Systemic lupus erythematosus	000	3
<i>CASR</i>	3q21.1	●							CMP-ab	7tm_3 ANF_receptor NCD3G	00000	45
<i>MYLK</i>	3q21.1	●●●							CMP-ab	I-sset Pkinase Pkinase_Tyr V-set ig	00000	34
<i>KPNA1</i>	3q21.1	●						✓	PPI-ab	5896, 7398, 672, 1434, 5897, 8543, 862	00	47
<i>ITGB5</i>	3q21.2	●●●							CMP-ab	EGF_2 Integrin_B_tail Integrin_b_cyt Integrin_beta	00000	7
<i>KALRN</i>	3q21.2	●●●	✓	✓	✓	✓	✓	✓	CMP-ab	I-sset V-set ig	00000	6
<i>UMPS</i>	3q21.2	●●●							CPS-s	Metabolic pathways	0000	1
<i>RASA2</i>	3q23	●							CMP-ab	C2 PH RasGAP	00000	70
<i>AGTR1</i>	3q24	●●			✓				CPS-ab	Angiotensin-converting enzyme 2 regulates heart function	00	6
<i>IGSF10</i>	3q25.1	●●							CMP-ab	I-sset V-set ig	00000	67
<i>MECOM</i>	3q26.2	●	✓	✓	✓	✓	✓	✓	CPS-ab	Pathways in cancer	0	5
<i>PLD1</i>	3q26.31	●	✓	✓	✓	✓	✓	✓	CPS-s	Metabolic pathways	0000	1
<i>KLHL6</i>	3q27.1	●			✓				CMP-ab	BACK BTB Kelch_1	00000	22
<i>KLHL24</i>	3q27.1	●							CMP-ab	BACK BTB Kelch_1 Kelch_2	00000	10
<i>EIF4G1</i>	3q27.1	●							CMP-ab	MA3 MIF4G W2	00000	33
<i>POLR2H</i>	3q27.1	●							CPS-s	Metabolic pathways	0000	1
<i>ALG3</i>	3q27.1	●							CPS-s	Metabolic pathways	0000	1
<i>EIF2B5</i>	3q27.1	●						✓	CPS-s	VEGF, Hypoxia, and Angiogenesis	0	4
<i>DVL3</i>	3q27.1	●						✓	CPS-ab	Pathways in cancer	0	9
<i>ST6GAL1</i>	3q27.3	●	✓	✓	✓	✓	✓	✓	CPS-s	Metabolic pathways	0000	1
<i>ADIPOQ</i>	3q27.3	●							CPS-s	Type II diabetes mellitus	00	4
<i>ADRA2C</i>	4p16.2	●						✓	CMP-ab	7TM_GPCR_Srsx 7TM_GPCR_Srx 7tm_1	00000	32
<i>HGFAC</i>	4p16.2	●							CMP-ab	EGF Kringle Trypsin fn1	00000	18
<i>PCDH7</i>	4p15.1	●			✓	✓			CMP-ab	Cadherin Cadherin_2 Protocadherin	00000	20
<i>PGM2</i>	4p14	●							CPS-s	Metabolic pathways	0000	1
<i>LIMCH1</i>	4p13	●	✓	✓	✓	✓	✓	✓	CMP-ab	CH	0000	18
<i>GNPDA2</i>	4p13	●●							CPS-s	Metabolic pathways	0000	1
<i>UCHL1</i>	4p13	●						✓	PPI-ab	3320, 1027, 10048, 23043, 7189, 3872	00	62
<i>KIT</i>	4q12	●			✓	✓			CPS-s	Cytokine-cytokine receptor interaction	000	2
<i>PDGFRA</i>	4q12	●			✓				CPS-s	Cytokine-cytokine receptor interaction	000	2
<i>IL21</i>	4q27	●						✓	CPS-s	Cytokine-cytokine receptor interaction	000	2
<i>IL2</i>	4q27	●						✓	CPS-s	Cytokine-cytokine receptor interaction	000	2
<i>FGF2</i>	4q28.1	●			✓				CPS-ab	Pathways in cancer	000	2
<i>SPATA5</i>	4q28.1	●						✓	PPI-ab	11137, 23560	0	347
<i>PDGFC</i>	4q32.1	●			✓				CPS-s	Cytokine-cytokine receptor interaction	000	2
<i>MFAP3L</i>	4q33	●●●●							CMP-ab	I-sset V-set ig	00000	34
<i>AADAT</i>	4q33	●●●●							CPS-s	Metabolic pathways	0000	1
<i>ACSL1</i>	4q35.1	●							CPS-s	Metabolic pathways	0000	1
<i>LPCAT1</i>	5p15.33	●						✓	CPS-s	Metabolic pathways	0000	1
<i>NDUFS6</i>	5p15.33	●			✓			✓	CPS-s	Metabolic pathways	0000	1
<i>SKP2</i>	5p13.2	●●			✓				CPS-ab	Pathways in cancer	000	2
<i>FGF10</i>	5p12	●●●●							CPS-ab	Melanoma	0	5
<i>ARL15</i>	5q11.2	●	✓	✓	✓	✓	✓	✓	CMP-ab	Arf Gtr1_RagA Miro Ras SRPRB	00000	4
<i>NDUFS4</i>	5q11.2	●							CPS-s	Metabolic pathways	0000	1
<i>HTR1A</i>	5q12.2	●			✓				CMP-ab	7tm_1	00000	25
<i>IQGAP2</i>	5q13.3	●	✓	✓	✓	✓	✓	✓	CMP-ab	CH	0000	18
<i>RASA1</i>	5q14.3	●			✓				CPS-s	Insulin Signaling Pathway	0	2
<i>COX7C</i>	5q14.3	●							CPS-s	Metabolic pathways	0000	1
<i>ERAP2</i>	5q15	●	✓	✓	✓	✓	✓	✓	CMP-ab	Peptidase_M1	0000	17
<i>ERAP1</i>	5q15	●			✓				PPI-ab	64167, 10564	0	36
<i>ST8SIA4</i>	5q21.1	●●●			✓				CPS-ab	Steps in the Glycosylation of Mammalian	000	3

											N-linked Oligosaccharides	
<i>MAN2A1</i>	5q21.3	●●	✓	✓	✓	✓	✓	✓	CPS-s	Metabolic pathways	○○○○	1
<i>CXCL14</i>	5q31.1	●							CPS-s	Cytokine-cytokine receptor interaction	○○○	2
<i>IL9</i>	5q31.1	●							CPS-s	Cytokine-cytokine receptor interaction	○○○	2
<i>TGFB1</i>	5q31.2	●		✓	✓	✓	✓	✓	CMP-ab	Fasciclin	○○○○	30
<i>SMAD5</i>	5q31.2	●			✓				CMP-ab	IRF-3 MH1 MH2	○○○○○	10
<i>C5orf4</i>	5q33.2	●							CPS-s	Metabolic pathways	○○○○	1
<i>GRM6</i>	5q35.3	●							CMP-ab	7tm_3 ANF_receptor NCD3G	○○○○○	45
<i>ADAMTS2</i>	5q35.3	●	✓	✓	✓	✓	✓	✓	CMP-ab	ADAM_spacer1 Pep_M12B_propep Reprolysin TSP_1	○○○○○	1
<i>CANX</i>	5q35.3	●							PPI-s	4018	○○○○	12
<i>BMP6</i>	6p24.3	●		✓	✓	✓	✓	✓	CPS-s	Cytokine-cytokine receptor interaction	○○○	2
<i>EDN1</i>	6p24.1	●							CPS-s	Hypoxia-Inducible Factor in the Cardiovascular System	○○	3
<i>MDGA1</i>	6p21.2	●	✓	✓	✓	✓	✓	✓	CMP-ab	I-sset V-set ig	○○○○○	6
<i>PIM1</i>	6p21.2	●							CPS-ab	Jak-STAT signaling pathway	○	10
<i>CAPN11</i>	6p21.1	●●							CMP-ab	Calpain_III Peptidase_C2	○○○○○	38
<i>AARS2</i>	6p21.1	●●							CMP-ab	tRNA-synt_2c tRNA_SAD	○○○○○	71
<i>VEGFA</i>	6p21.1	●●							CPS-s	Hypoxia-Inducible Factor in the Cardiovascular System	○○	2
<i>POLR1C</i>	6p21.1	●●							CPS-s	Metabolic pathways	○○○○	1
<i>HSP90AB1</i>	6p21.1	●●							PPI-s	3667	○○○○	2
<i>XPO5</i>	6p21.1	●●							PPI-ab	4609, 8793	○○	406
<i>SUPT3H</i>	6p12.3	●			✓				PPI-ab	1105, 4609, 10474, 6883	○	67
<i>EYS</i>	6q12	●	✓	✓	✓	✓	✓	✓	CMP-ab	EGF Laminin_G_1 Laminin_G_2	○○○○○	3
<i>FUT9</i>	6q16.1	●●●●	✓	✓	✓	✓	✓	✓	CPS-s	Metabolic pathways	○○○○	1
<i>GRIK2</i>	6q16.3	●			✓				CMP-ab	ANF_receptor Lig_chan Lig_chan-Glu_bd SBP_bac_3	○○○○○	3
<i>WASF1</i>	6q21	●			✓				CPS-ab	Rac 1 cell motility signaling pathway	○○○	5
<i>RSPO3</i>	6q22.33	●		✓	✓	✓	✓	✓	CMP-ab	TSP_1	○○○○	31
<i>SGK1</i>	6q23.2	●				✓	✓	✓	CMP-ab	Pkinase Pkinase_C Pkinase_Tyr	○○○○○	77
<i>LRP11</i>	6q25.1	●	✓	✓	✓	✓	✓	✓	CMP-s	4040 Ldl_recept_a	●●	1
<i>KATNA1</i>	6q25.1	●							CMP-ab	AAA AAA_2 RuvB_N Vps4_C	○○○○○	11
<i>MTHFD1L</i>	6q25.1	●●●	✓	✓	✓	✓	✓	✓	CPS-s	Metabolic pathways	○○○○	1
<i>LATS1</i>	6q25.1	●							PPI-ab	4609, 3984, 5879	○	106
<i>SYNE1</i>	6q25.2	●	✓	✓	✓	✓	✓	✓	CMP-ab	CH	○○○○	18
<i>ACAT2</i>	6q25.3	●							CPS-s	Metabolic pathways	○○○○	1
<i>PLG</i>	6q26	●							CMP-s	4018 DUF1986 Kringle Trypsin	●●●●	1
<i>LPA</i>	6q26	●							CMP-ab	DUF1986 Kringle Trypsin	○○○○○	53
<i>AGPAT4</i>	6q26	●							CPS-s	Metabolic pathways	○○○○	1
<i>RAC1</i>	7p22.1	●			✓				CPS-s	Phagosome	○	3
<i>CYTH3</i>	7p22.1	●			✓	✓	✓	✓	CPS-ab	ADP-sRibosylation Factor	○○○	3
<i>EIF2AK1</i>	7p22.1	●							CPS-ab	Regulation of eIF2	○	14
<i>DGKB</i>	7p21.2	●			✓	✓	✓	✓	CPS-s	Metabolic pathways	○○○○	1
<i>RALA</i>	7p14.1	●							CMP-ab	Arf GTP_EFTU Miro Ras	○○○○○	30
<i>DDX56</i>	7p13	●	✓	✓	✓	✓	✓	✓	CMP-ab	DEAD Helicase_C ResIII	○○○○○	21
<i>TBRG4</i>	7p13	●							CMP-ab	FAST_1 FAST_2 RAP	○○○○○	23
<i>OGDH</i>	7p13	●	✓	✓	✓	✓	✓	✓	CPS-s	Metabolic pathways	○○○○	1
<i>PGAM2</i>	7p13	●							CPS-s	Metabolic pathways	○○○○	1
<i>POLD2</i>	7p13	●							CPS-s	Metabolic pathways	○○○○	1
<i>GCK</i>	7p13	●							CPS-s	Metabolic pathways	○○○○	1
<i>CAMK2B</i>	7p13	●							CPS-ab	Olfactory transduction	○○○○	1
<i>H2AFV</i>	7p13	●			✓				CPS-ab	Systemic lupus erythematosus	○○	3
7q11.2												
<i>LIMK1</i>	7q11.23	●●●							CPS-ab	Rac 1 cell motility signaling pathway	○○	5
<i>LAT2</i>	7q11.23	●●●				✓	✓	✓	PPI-ab	5336, 2885	○○	6
<i>CD36</i>	7q21.11	●●				✓	✓	✓	CPS-s	Phagosome	○	3
<i>SEMA3A</i>	7q21.11	●			✓	✓	✓	✓	CPS-ab	Axon guidance	○○○	1
<i>SEMA3C</i>	7q21.11	●●	✓	✓	✓	✓	✓	✓	CPS-ab	Axon guidance	○○○	2
7q21.3												
<i>PON1</i>	7q21.3	-										
<i>PON2</i>	7q21.3	-										
<i>RELN</i>	7q22.1	●	✓	✓	✓	✓	✓	✓	CPS-s	ECM-receptor interaction	○	1
<i>DOCK4</i>	7q31.1	●	✓	✓	✓	✓	✓	✓	CMP-ab	Ded_cyto	○○○○	16
<i>BPGM</i>	7q33	●			✓	✓	✓	✓	CPS-s	Metabolic pathways	○○○○	1
<i>AKR1B10</i>	7q33	●							CPS-s	Metabolic pathways	○○○○	1
<i>AKR1B1</i>	7q33	●				✓	✓	✓	CPS-s	Metabolic pathways	○○○○	1
7q36												
<i>ABP1</i>	7q36.1	●			✓	✓	✓	✓	CMP-ab	Cu_amine_oxid Cu_amine_oxidN2 Cu_amine_oxidN3	○○○○○	19
<i>FASTK</i>	7q36.1	●							CMP-ab	FAST_1 FAST_2 RAP	○○○○○	23

<i>NOS3</i>	7q36.1	•				✓	✓	CPS-s	Metabolic pathways	0000	1
<i>ATP6V0E2</i>	7q36.1	•					✓	CPS-s	Metabolic pathways	0000	1
<i>CHPF2</i>	7q36.1	•					✓	CPS-s	Metabolic pathways	0000	1
<i>ABCF2</i>	7q36.1	•					✓	PPI-ab	6157, 84940	000	234
<i>SHH</i>	7q36.3	•		✓			✓	CPS-ab	Pathways in cancer	000	2
<i>ASAH1</i>	8p22	•				✓	✓	CPS-s	Metabolic pathways	0000	1
<i>NAT1</i>	8p22	•		✓		✓	✓	CPS-s	Metabolic pathways	0000	1
<i>NAT2</i>	8p22	•				✓	✓	CPS-s	Metabolic pathways	0000	1
<i>TUSC3</i>	8p22	••		✓				CPS-ab	N-Glycan biosynthesis	0	12
8p21-p12											
<i>TNFRSF10D</i>	8p21.3	•					✓	CPS-s	Cytokine-cytokine receptor interaction	000	2
<i>TNFRSF10A</i>	8p21.3	•				✓	✓	CPS-s	Cytokine-cytokine receptor interaction	000	2
<i>TNFRSF10C</i>	8p21.3	•					✓	CPS-s	Cytokine-cytokine receptor interaction	000	2
<i>TNFRSF10B</i>	8p21.3	•					✓	CPS-s	Cytokine-cytokine receptor interaction	000	2
<i>ZNF703</i>	8p12	•		✓			✓	CMP-ab	nlz1	0000	78
<i>ANK1</i>	8p11.21	•					✓	CMP-ab	Ank Death ZU5	00000	60
<i>IKBKB</i>	8p11.21	•		✓		✓	✓	CPS-s	Type II diabetes mellitus	0	1
									Platelet Amyloid Precursor Protein		
<i>PLAT</i>	8p11.21	•		✓	✓	✓	✓	CPS-ab	Pathway	00	2
<i>JPH1</i>	8q21.11	•		✓	✓	✓	✓	PPI-ab	4088	0	5
<i>ATP6V0D2</i>	8q21.3	•		✓	✓	✓	✓	CPS-s	Metabolic pathways	0000	1
<i>RUNX1T1</i>	8q21.3	•					✓	CPS-ab	Pathways in cancer	0	9
<i>SQLE</i>	8q24.13	•					✓	CPS-s	Metabolic pathways	0000	1
<i>MYC</i>	8q24.21	•				✓	✓	CPS-ab	Pathways in cancer	000	2
<i>ST3GAL1</i>	8q24.22	•				✓	✓	CPS-s	Metabolic pathways	0000	1
<i>BAI1</i>	8q24.3	••		✓	✓		✓	CMP-ab	7tm_2 DUF3497 GPS	00000	4
<i>JRK</i>	8q24.3	•					✓	CMP-ab	CENP-sB_N DDE Transposase_Tc5	00000	29
<i>TIGD5</i>	8q24.3	•					✓	CMP-ab	CENP-sB_N DDE Transposase_Tc5	00000	29
<i>CYP11B2</i>	8q24.3	•					✓	CPS-s	Metabolic pathways	0000	1
<i>CYP11B1</i>	8q24.3	•					✓	CPS-s	Metabolic pathways	0000	1
<i>PYCR1</i>	8q24.3	•					✓	CPS-s	Metabolic pathways	0000	1
<i>NAPRT1</i>	8q24.3	•					✓	CPS-s	Metabolic pathways	0000	1
<i>TSTA3</i>	8q24.3	•					✓	CPS-s	Metabolic pathways	0000	1
<i>MAFA</i>	8q24.3	•				✓	✓	CPS-s	Type II diabetes mellitus	00	4
<i>ARC</i>	8q24.3	••			✓	✓	✓	PPI-ab	3866, 2904	0	210
<i>DOCK8</i>	9p24.3	•		✓	✓	✓	✓	CMP-ab	Ded_cyto	0000	16
<i>CD274</i>	9p24.1	•					✓	CMP-ab	C1-set C2-set_2 V-set ig	00000	41
<i>JAK2</i>	9p24.1	•					✓	PPI-s	3667	0000	8
<i>MTAP</i>	9p21.3	••••				✓	✓	CPS-s	Metabolic pathways	0000	1
<i>CDKN2A</i>	9p21.3	••••				✓	✓	CPS-ab	Non-small cell lung cancer	0	6
<i>CDKN2B</i>	9p21.3	••••		✓	✓	✓	✓	CPS-ab	Pathways in cancer	000	2
9q22-q31											
<i>CORO2A</i>	9q22.33	••		✓	✓	✓	✓	CMP-ab	DUF1899 DUF1900 WD40	00000	6
<i>NANS</i>	9q22.33	••				✓	✓	CPS-s	Metabolic pathways	0000	1
<i>TRIM14</i>	9q22.33	••				✓	✓	PPI-ab	2885	0	14
									6780, 3187, 6632, 5395, 1982, 1981, 8175, 23008, 84078, 26512	00	158
<i>NCBP1</i>	9q22.33	••					✓	PPI-ab			
<i>ABCA1</i>	9q31.2	-									
<i>EPB41LAB</i>	9q31.3	•					✓	CMP-ab	FA FERM_C FERM_M FERM_N	00000	15
<i>PTPN3</i>	9q31.3	•					✓	CMP-ab	FERM_C FERM_M FERM_N	00000	40
<i>UGCG</i>	9q31.3	•		✓	✓	✓	✓	CPS-s	Metabolic pathways	0000	1
<i>IKBKAP</i>	9q31.3	•		✓	✓	✓	✓	CPS-ab	CD40L Signaling Pathway	00	7
<i>PTGS1</i>	9q33.2	••					✓	CPS-s	Metabolic pathways	0000	1
<i>OR1B1</i>	9q33.2	••			✓	✓	✓	CPS-ab	Olfactory transduction	000	1
<i>OR1L3</i>	9q33.2	••		✓	✓	✓	✓	CPS-ab	Olfactory transduction	000	1
<i>OR1L4</i>	9q33.2	••				✓	✓	CPS-ab	Olfactory transduction	0	5
<i>OR1L1</i>	9q33.2	••				✓	✓	CPS-ab	Olfactory transduction	0	5
<i>OR1J1</i>	9q33.2	••					✓	CPS-ab	Olfactory transduction	0000	1
<i>OR1Q1</i>	9q33.2	••					✓	CPS-ab	Olfactory transduction	0000	1
<i>OR1K1</i>	9q33.2	••					✓	CPS-ab	Olfactory transduction	0000	1
<i>OR5C1</i>	9q33.2	••					✓	CPS-ab	Olfactory transduction	0000	1
<i>OR1L8</i>	9q33.2	••					✓	CPS-ab	Olfactory transduction	0000	1
<i>OR1J2</i>	9q33.2	••					✓	CPS-ab	Olfactory transduction	0000	1
<i>OR1N2</i>	9q33.2	••					✓	CPS-ab	Olfactory transduction	0000	1
<i>OR1N1</i>	9q33.2	••					✓	CPS-ab	Olfactory transduction	0000	1
<i>OR1J4</i>	9q33.2	••					✓	CPS-ab	Olfactory transduction	0000	1
<i>OR1L6</i>	9q33.2	••					✓	CPS-ab	Olfactory transduction	0000	1
									26227, 3861, 3690, 3689, 3320, 3326, 3868, 3860, 5870, 3187, 5245, 3857, 6155, 6632, 6229, 6160, 2969, 3192, 6128, 708, 6429, 3757, 11137, 25902,	0	51
<i>RABGAP1</i>	9q33.2	••					✓	PPI-ab			

										6601, 51493, 3688			
<i>ADAMTSL2</i>	9q34.2	●						✓	CMP-ab	ADAM_spacer1 PLAC TSP_1	ooooo	38	
<i>ADARB2</i>	10p15.3	●	✓	✓	✓	✓	✓	✓	CMP-ab	A_deamin dsrm	ooooo	4	
<i>IDI2</i>	10p15.3	●						✓	CPS-s	Metabolic pathways	0000	1	
<i>IDI1</i>	10p15.3	●						✓	CPS-s	Metabolic pathways	0000	1	
<i>FRMD4A</i>	10p13	●	✓	✓	✓	✓	✓	✓	CMP-ab	FERM_C FERM_M FERM_N	ooooo	2	
<i>NRP1</i>	10p11.22	●		✓	✓	✓	✓	✓	CPS-ab	Axon guidance	000	1	
<i>ITGB1</i>	10p11.22	●						✓	PPI-s	948	0000	9	
<i>PRKG1</i>	10q21.1	●	✓	✓	✓	✓	✓	✓	CPS-ab	Olfactory transduction	000	1	
<i>ANK3</i>	10q21.2	●	✓	✓	✓	✓	✓	✓	CMP-ab	Ank Death ZU5	ooooo	60	
<i>CTNNA3</i>	10q21.3	●	✓	✓	✓	✓	✓	✓	CPS-ab	Adherens junction	000	1	
<i>ZNF503</i>	10q22.2	●						✓	CMP-ab	nlz1	oooo	78	
<i>POLR3A</i>	10q22.3	●	✓	✓	✓	✓	✓	✓	CPS-s	Metabolic pathways	0000	1	
<i>TNKS2</i>	10q23.32	●●						✓	CMP-ab	Ank SAM_1 SAM_2	ooooo	7	
<i>SORBS1</i>	10q23.33	●●	✓	✓	✓	✓	✓	✓	CPS-s	Insulin signaling pathway	0	1	
<i>ALDH18A1</i>	10q23.33	●●						✓	CPS-s	Metabolic pathways	0000	1	
<i>CYP2C9</i>	10q23.33	●●						✓	CPS-s	Metabolic pathways	0000	1	
<i>CYP2C8</i>	10q23.33	●●						✓	CPS-s	Metabolic pathways	0000	1	
<i>PNLIP</i>	10q25.3	●						✓	CPS-s	Metabolic pathways	0000	1	
<i>PNLIPRP3</i>	10q25.3	●						✓	CPS-s	Metabolic pathways	0000	1	
<i>TH</i>	11p15.5	●						✓	CPS-s	Metabolic pathways	0000	1	
<i>INS</i>	11p15.5	●						✓	CPS-s	Type II diabetes mellitus	00	4	
<i>SBF2</i>	11p15.4	●						✓	CMP-ab	DENN dDENN uDENN	ooooo	35	
<i>ST5</i>	11p15.4	●						✓	CMP-ab	DENN dDENN uDENN	ooooo	35	
<i>TRIM6</i>	11p15.4	●						✓	CMP-ab	SPRY zf-B_box zf-C3HC4	ooooo	33	
<i>TRIM5</i>	11p15.4	●	✓	✓	✓	✓	✓	✓	CMP-ab	SPRY zf-B_box zf-C3HC4	ooooo	10	
<i>TRIM22</i>	11p15.4	●						✓	CMP-ab	SPRY zf-B_box zf-C3HC4	ooooo	10	
<i>TRIM6-TRIM34</i>	11p15.4	●						✓	CMP-ab	SPRY zf-B_box zf-C3HC4	ooooo	10	
<i>TRIM34</i>	11p15.4	●						✓	CMP-ab	SPRY zf-B_box zf-C3HC4	ooooo	10	
<i>AMPD3</i>	11p15.4	●	✓	✓	✓	✓	✓	✓	CPS-s	Metabolic pathways	0000	1	
<i>OR10A3</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	2	
<i>OR10A6</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	2	
<i>OR56A5</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	2	
<i>OR56A1</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	2	
<i>OR56A3</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	2	
<i>OR5P3</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	2	
<i>OR51V1</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	2	
<i>OR51M1</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	2	
<i>OR56A4</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	2	
<i>OR51B4</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	2	
<i>OR56B4</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	2	
<i>OR51B2</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	2	
<i>OR51B6</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	2	
<i>OR5P2</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	2	
<i>OR52L1</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	2	
<i>OR51Q1</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	2	
<i>OR52B2</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	2	
<i>OR51B5</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	2	
<i>OR52E8</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	1	
<i>OR52E6</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	1	
<i>OR52B6</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	1	
<i>OR52N1</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	1	
<i>OR56B1</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	1	
<i>OR52N2</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	1	
<i>OR52E4</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	1	
<i>OR51I1</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	1	
<i>OR51I2</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	1	
<i>OR52D1</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	1	
<i>OR52N5</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	1	
<i>OR52H1</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	1	
<i>OR52N4</i>	11p15.4	●						✓	CPS-ab	Olfactory transduction	0000	1	
<i>KCNQ1</i>	11p15.4	●	✓	✓	✓	✓	✓	✓	CPS-ab	Vibrio cholerae infection	00	3	
<i>PARVA</i>	11p15.3	●●●●	✓	✓	✓	✓	✓	✓	CMP-ab	CH	oooo	18	
<i>MICAL2</i>	11p15.3	●●●●	✓	✓	✓	✓	✓	✓	CMP-ab	CH	oooo	18	
<i>EIF4G2</i>	11p15.3	●						✓	CMP-ab	MA3 MIF4G W2	ooooo	33	
<i>CTR9</i>	11p15.3	●						✓	PPI-ab	80349	0000	204	
<i>MYOD1</i>	11p15.1	●						✓	CMP-ab	Basic HLH Myf5	ooooo	11	
<i>OTOG</i>	11p15.1	●						✓	CMP-ab	C8 TIL VWWD	ooooo	9	
<i>KCNC1</i>	11p15.1	●						✓	CMP-ab	Ion_trans Ion_trans_2 K_tetra	ooooo	56	
<i>PIK3C2A</i>	11p15.1	●						✓	CPS-s	Metabolic pathways	0000	1	

<i>KCNJ11</i>	11p15.1	●				✓	✓	CPS-s	Type II diabetes mellitus	00	4
<i>ABCC8</i>	11p15.1	●				✓	✓	CPS-s	Type II diabetes mellitus	00	4
<i>USH1C</i>	11p15.1	●	✓	✓	✓	✓	✓	CPS-ab	Chaperones modulate interferon Signaling Pathway	0	11
<i>LDLRAD3</i>	11p13	●						CMP-s	4040 Ldl_recept_a	●●	6
<i>CAT</i>	11p13	●				✓	✓	CPS-s	Metabolic pathways	0000	1
<i>APIP</i>	11p13	●				✓		CPS-s	Metabolic pathways	0000	1
<i>PDHX</i>	11p13	●					✓	CPS-s	Metabolic pathways	0000	1
<i>TRAF6</i>	11p12	●					✓	CPS-ab	Toxoplasmosis	00	4
<i>EXT2</i>	11p11.2	●	✓	✓	✓	✓	✓	CPS-s	Metabolic pathways	0000	1
<i>HSD17B12</i>	11p11.2	●					✓	CPS-s	Metabolic pathways	0000	1
<i>CD82</i>	11p11.2	●					✓	PPI-ab	3689, 3688, 4179, 2065, 3675, 4927, 23118, 821	00	107
<i>MS4A2</i>	11q12.1	●				✓	✓	PPI-ab	2885, 3320	0	52
<i>CORO1B</i>	11q13.1	●					✓	CMP-ab	DUF1899 DUF1900 WD40	00000	43
<i>RPS6KB2</i>	11q13.1	●					✓	CMP-ab	Pkinase Pkinase_C Pkinase_Tyr	00000	77
<i>RPS6KA4</i>	11q13.1	●					✓	CMP-ab	Pkinase Pkinase_C Pkinase_Tyr	00000	77
<i>CLCF1</i>	11q13.1	●					✓	CPS-s	Cytokine-cytokine receptor interaction	000	2
<i>VEGFB</i>	11q13.1	●				✓	✓	CPS-s	Cytokine-cytokine receptor interaction	000	2
<i>COX8A</i>	11q13.1	●				✓	✓	CPS-s	Metabolic pathways	0000	1
<i>POLD4</i>	11q13.1	●					✓	CPS-s	Metabolic pathways	0000	1
<i>PLCB3</i>	11q13.1	●					✓	CPS-s	Metabolic pathways	0000	1
<i>AIP</i>	11q13.1	●					✓	CPS-ab	Ahr Signal Transduction Pathway	0	10
<i>TRMT112</i>	11q13.1	●					✓	PPI-ab	10474, 2035, 7428, 7327, 23043, 7189	0	190
<i>MACROD1</i>	11q13.1	●	✓	✓	✓	✓	✓	PPI-ab	2035	0	10
<i>ALDH3B2</i>	11q13.2	●				✓	✓	CPS-s	Metabolic pathways	0000	1
<i>NDUFV1</i>	11q13.2	●				✓	✓	CPS-s	Metabolic pathways	0000	1
<i>CHKA</i>	11q13.2	●					✓	CPS-s	Metabolic pathways	0000	1
<i>TCIRG1</i>	11q13.2	●					✓	CPS-s	Metabolic pathways	0000	1
<i>ALDH3B1</i>	11q13.2	●					✓	CPS-s	Metabolic pathways	0000	1
<i>NDUFS8</i>	11q13.2	●					✓	CPS-s	Metabolic pathways	0000	1
<i>GSTP1</i>	11q13.2	●				✓	✓	CPS-ab	Pathways in cancer	0	9
<i>SHANK2</i>	11q13.3	●				✓	✓	CMP-ab	SAM_1 SAM_2 SH3_2	00000	37
<i>RAB6A</i>	11q13.4	●●	✓	✓	✓	✓	✓	CMP-ab	Arf Gtr1_RagA Miro Ras	00000	11
<i>RELT</i>	11q13.4	●●				✓	✓	CPS-s	Cytokine-cytokine receptor interaction	000	2
<i>NADSYN1</i>	11q13.4	●				✓	✓	CPS-s	Metabolic pathways	0000	1
<i>DHCR7</i>	11q13.4	●					✓	CPS-s	Metabolic pathways	0000	1
<i>GRIA4</i>	11q22.3	●					✓	CMP-ab	ANF_receptor Lig_chan Lig_chan-Glu_bd SBP_bac_3	00000	13
<i>KBTBD3</i>	11q22.3	●				✓	✓	CMP-ab	BACK BTB Kelch_1	00000	22
<i>RDX</i>	11q22.3	●				✓	✓	CMP-ab	FERM_C FERM_M FERM_N	00000	14
11q23											
<i>MMP3</i>	11q22.3	-									
<i>APOA1</i>	11q23.3	●					✓	PPI-s	19, 5444	000	13
<i>OR8D4</i>	11q24.1	●				✓	✓	CPS-ab	Olfactory transduction	000	1
<i>OR10G9</i>	11q24.1	●					✓	CPS-ab	Olfactory transduction	0000	2
<i>OR10G4</i>	11q24.1	●					✓	CPS-ab	Olfactory transduction	0000	2
<i>OR4D5</i>	11q24.1	●					✓	CPS-ab	Olfactory transduction	0000	2
<i>OR10G7</i>	11q24.1	●					✓	CPS-ab	Olfactory transduction	0000	2
<i>OR6T1</i>	11q24.1	●					✓	CPS-ab	Olfactory transduction	0000	2
<i>OR10G8</i>	11q24.1	●					✓	CPS-ab	Olfactory transduction	0000	2
<i>OR10S1</i>	11q24.1	●					✓	CPS-ab	Olfactory transduction	0000	2
<i>OR6M1</i>	11q24.1	●				✓	✓	CPS-ab	Olfactory transduction	0000	1
<i>OR6X1</i>	11q24.1	●					✓	CPS-ab	Olfactory transduction	0000	1
<i>ROBO4</i>	11q24.2	●					✓	CMP-ab	I-sset fn3 ig	00000	39
<i>HEPACAM</i>	11q24.2	●	✓			✓	✓	CMP-ab	I-sset V-set ig	00000	28
<i>VSIG2</i>	11q24.2	●					✓	CMP-ab	I-sset V-set ig	00000	67
<i>STT3A</i>	11q24.2	●					✓	CPS-s	Metabolic pathways	0000	1
<i>ROBO3</i>	11q24.2	●					✓	CPS-ab	Axon guidance	0	15
<i>JAM3</i>	11q25	●●				✓	✓	CMP-ab	C2-set_2 I-sset V-set ig	00000	17
<i>IGSF9B</i>	11q25	●●					✓	CMP-ab	I-sset V-set fn3 ig	00000	21
<i>ACAD8</i>	11q25	●●					✓	CPS-s	Metabolic pathways	0000	1
<i>B3GAT1</i>	11q25	●●					✓	CPS-s	Metabolic pathways	0000	1
12p13.3-p11.2											
<i>DDX47</i>	12p13.1	●				✓	✓	CMP-ab	DEAD Helicase_C ResIII	00000	26
<i>CDKN1B</i>	12p13.1	●					✓	CPS-ab	Pathways in cancer	0	9
<i>GRIN2B</i>	12p13.1	●	✓	✓		✓	✓	PPI-s	3667	000	4
<i>LRP6</i>	12p13.2	●					✓	-	-		
<i>PIK3C2G</i>	12p12.3	●				✓	✓	CPS-s	Metabolic pathways	0000	1
<i>PLCZ1</i>	12p12.3	●				✓	✓	CPS-s	Metabolic pathways	0000	1
<i>BCAT1</i>	12p12.1	●				✓	✓	CPS-s	Metabolic pathways	0000	1

<i>KRAS</i>	12p12.1	●			✓	✓	CPS-ab	Pathways in cancer	0	9	
<i>CNTN1</i>	12q12	●			✓	✓	CMP-ab	I-sset V-set fn3 ig	00000	21	
<i>ERBB3</i>	12q13.2	●●			✓	✓	CMP-ab	Furin-like Pkinase Pkinase_Tyr Recep_L_domain	00000	12	
<i>MMP19</i>	12q13.2	●●				✓	CMP-ab	Hemopexin PG_binding_1 Peptidase_M10	00000	37	
<i>IL23A</i>	12q13.2	●●			✓	✓	CPS-s	Cytokine-cytokine receptor interaction	000	2	
<i>CS</i>	12q13.2	●●		✓	✓	✓	CPS-s	Metabolic pathways	0000	1	
<i>GLS2</i>	12q13.2	●●			✓	✓	CPS-s	Metabolic pathways	0000	1	
<i>DGKA</i>	12q13.2	●●				✓	CPS-s	Metabolic pathways	0000	1	
<i>STAT2</i>	12q13.2	●●			✓	✓	CPS-ab	Jak-STAT signaling pathway	0	10	
<i>RAB5B</i>	12q13.2	●●				✓	CPS-ab	Tuberculosis	000	5	
								8317, 2806, 2035, 5898, 4654, 7507, 5583, 898, 5037, 471, 672, 7428, 4332, 1027, 902, 5499, 4088, 5888, 8208, 6502, 80018, 11140, 124930, 192111, 6272,			
<i>CDK2</i>	12q13.2	●●				✓	PPI-ab	84811, 5425, 7290, 3398, 932, 988, 1045	0	17	
<i>ATP5B</i>	12q13.3	●●				✓	CPS-s	Metabolic pathways	0000	1	
<i>PRIM1</i>	12q13.3	●●				✓	CPS-s	Metabolic pathways	0000	1	
<i>SRGAP1</i>	12q14.2	●			✓	✓	CPS-ab	Axon guidance	0	15	
<i>OTOGL</i>	12q21.31	●				✓	CMP-ab	AbfB C8 TIL VWD	00000	8	
<i>MYF5</i>	12q21.31	●		✓	✓	✓	✓	CMP-ab	Basic HLH Myf5	00000	11
<i>ACSS3</i>	12q21.31	●			✓	✓	CPS-s	Metabolic pathways	0000	1	
<i>LIN7A</i>	12q21.31	●			✓	✓	✓	CPS-ab	Chaperones modulate interferon Signaling Pathway	0	11
<i>PRDM4</i>	12q23.3	●			✓	✓	✓	PPI-ab	54855, 4088	000	16
<i>ACAD10</i>	12q24.12	●				✓	CMP-ab	Acyl-CoA_dh_1 Acyl-CoA_dh_2 Acyl-CoA_dh_M Acyl-CoA_dh_N	00000	9	
<i>ALDH2</i>	12q24.12	●			✓	✓	CPS-s	Metabolic pathways	0000	1	
<i>PTPN11</i>	12q24.13	●				✓	CPS-ab	Jak-STAT signaling pathway	0	10	
<i>VSIG10</i>	12q24.23	●				✓	CMP-ab	I-sset V-set ig	00000	67	
<i>POLE</i>	12q24.33	●				✓	CPS-s	Metabolic pathways	0000	1	
<i>FZD10</i>	12q24.33	●●		✓		✓	CPS-ab	Pathways in cancer	000	2	
								13q12			
<i>CRYL1</i>	13q12.11	●				✓	CPS-s	Metabolic pathways	0000	1	
<i>FLT3</i>	13q12.2	●		✓	✓	✓	✓	CPS-s	Cytokine-cytokine receptor interaction	000	2
<i>PRHOXNB</i>	13q12.2	●				✓	✓	CPS-s	Metabolic pathways	0000	1
<i>POLR1D</i>	13q12.2	●				✓	✓	CPS-s	Metabolic pathways	0000	1
<i>PDX1</i>	13q12.2	●				✓	✓	CPS-s	Type II diabetes mellitus	00	4
<i>CDX2</i>	13q12.2	●				✓	✓	MIR-ab	MI0000270	00	1
<i>KATNAL1</i>	13q12.3	●				✓	CMP-ab	AAA AAA_2 RuvB_N Vps4_C	00000	11	
<i>FLT1</i>	13q12.3	●				✓	CPS-s	Cytokine-cytokine receptor interaction	000	2	
<i>ALOX5AP</i>	13q12.3	●		✓	✓	✓	✓	CPS-ab	Eicosanoid Metabolism	0	5
<i>KL</i>	13q13.1	-									
<i>POSTN</i>	13q13.3	●		✓	✓	✓	✓	CMP-ab	Fasciclin	0000	30
<i>KBTBD6</i>	13q14.11	●				✓	CMP-ab	BACK BTB Kelch_1	00000	50	
<i>KBTBD7</i>	13q14.11	●				✓	CMP-ab	BACK BTB Kelch_1	00000	50	
<i>DGKH</i>	13q14.11	●				✓	CPS-s	Metabolic pathways	0000	1	
<i>ALG11</i>	13q14.3	●●				✓	CPS-s	Metabolic pathways	0000	1	
<i>PCDH9</i>	13q21.32	●			✓	✓	✓	CMP-ab	Cadherin Cadherin_2 Protocadherin	00000	20
								7TM_GPCR_Srsx 7TM_GPCR_Srx			
<i>EDNRB</i>	13q22.3	●		✓	✓	✓	✓	CMP-ab	7tm_1	00000	8
<i>FARP1</i>	13q32.2	●		✓	✓	✓	✓	CMP-ab	FERM_C FERM_M FERM_N	00000	2
<i>IPO5</i>	13q32.2	●				✓	✓	PPI-ab	5897, 3021, 1778, 5108, 54606	00	31
<i>IRS2</i>	13q34	●●		✓	✓	✓	✓	CMP-s	3667 IRS PH	●●●	1
<i>RAB20</i>	13q34	●				✓	✓	CMP-ab	Arf Miro Ras	00000	24
<i>COL4A2</i>	13q34	●●		✓	✓	✓	✓	CPS-s	ECM-receptor interaction	0	1
<i>COL4A1</i>	13q34	●●				✓	✓	CPS-ab	Pathways in cancer	000	2
<i>ING1</i>	13q34	●				✓	✓	PPI-ab	10971, 6601	0	457
<i>NID2</i>	14q22.1	●			✓	✓	✓	CMP-s	4040 Ldl_recept_b	●●●	3
								7TM_GPCR_Srsx 7TM_GPCR_Srx			
<i>PTGER2</i>	14q22.1	●				✓	CMP-ab	7tm_1	00000	65	
<i>FRMD6</i>	14q22.1	●				✓	✓	CMP-ab	FERM_C FERM_M FERM_N	00000	18
<i>PRKCH</i>	14q23.1	●			✓	✓	✓	CMP-ab	C1_1 Pkinase Pkinase_C Pkinase_Tyr	00000	13
								Hypoxia-Inducible Factor in the			
<i>HIF1A</i>	14q23.2	●				✓	✓	CPS-s	Cardiovascular System	00	2
<i>DYNC1H1</i>	14q32.31	●		✓	✓	✓	✓	CPS-s	Phagosome	0	3
<i>HSP90AA1</i>	14q32.31	●				✓	✓	PPI-s	4846	000	2
<i>CDC42BPB</i>	14q32.32	●			✓	✓	✓	CMP-ab	C1_1 Pkinase Pkinase_C Pkinase_Tyr	00000	13
<i>TRAF3</i>	14q32.32	●				✓	✓	CPS-ab	CD40L Signaling Pathway	00	7
<i>EIF5</i>	14q32.32	●				✓	✓	CPS-ab	Regulation of eIF2	0	14
<i>CKB</i>	14q32.33	●				✓	CPS-s	Metabolic pathways	0000	1	

<i>SPINT1</i>	15q15.1	●					✓	CMP-s	4040 Ldl_recept_a	●●	5
<i>IVD</i>	15q15.1	●				✓	✓	CPS-s	Metabolic pathways	0000	1
<i>PLCB2</i>	15q15.1	●					✓	CPS-s	Metabolic pathways	0000	1
<i>EIF2AK4</i>	15q15.1	●					✓	CPS-ab	Regulation of eIF2	0	14
<i>PAK6</i>	15q15.1	●					✓	CPS-ab	Renal cell carcinoma	0	13
<i>RAD51</i>	15q15.1	●					✓	PPI-s	3667	0000	6
<i>CASC5</i>	15q15.1	●					✓	PPI-ab	5499, 79003, 79980	0	251
<i>SEMA6D</i>	15q21.1	●	✓	✓	✓	✓	✓	CPS-ab	Axon guidance	000	2
<i>LCTL</i>	15q22.31	●					✓	CMP-s	9365 Glyco_hydro_1	●	8
<i>RASL12</i>	15q22.31	●●	✓	✓	✓	✓	✓	CMP-ab	Arf Miro Ras	00000	24
<i>IGDCC4</i>	15q22.31	●●					✓	CMP-ab	I-sset fn3 ig	00000	76
<i>IGDCC3</i>	15q22.31	●●					✓	CMP-ab	I-sset V-set fn3 ig	00000	46
<i>PLEKH02</i>	15q22.31	●●					✓	CPS-s	Cytokine-cytokine receptor interaction	000	2
<i>MTFMT</i>	15q22.31	●●					✓	CPS-ab	One carbon pool by folate	000	1
<i>SMAD3</i>	15q22.33	●	✓	✓	✓	✓	✓	PPI-s	3667	000	3
<i>THSD4</i>	15q23	●	✓	✓	✓	✓	✓	CMP-ab	ADAM_spacer1 TSP_1	00000	5
<i>PSTPIP1</i>	15q24.3	●					✓	CMP-ab	FCH SH3_1 SH3_2 ADAM_spacer1 Pep_M12B_propep	00000	36
<i>ADAMTS7</i>	15q25.1	●●	✓	✓	✓	✓	✓	CMP-ab	Reprolysin TSP_1	00000	1
<i>PSMA4</i>	15q25.1	●●	✓	✓	✓	✓	✓	CMP-ab	Proteasome Proteasome_A_N	00000	6
<i>ACSBG1</i>	15q25.1	●●					✓	CPS-s	Metabolic pathways	0000	1
<i>FAH</i>	15q25.1	●	✓	✓	✓	✓	✓	CPS-s	Metabolic pathways	0000	1
<i>IDH3A</i>	15q25.1	●●					✓	CPS-s	Metabolic pathways	0000	1
<i>MTHFS</i>	15q25.1	●					✓	CPS-s	Metabolic pathways	0000	1
<i>ARNT2</i>	15q25.1	●					✓	CPS-ab	Pathways in cancer	0	9
<i>WDR61</i>	15q25.1	●●					✓	CPS-ab	RNA degradation	00	6
ACAN	15q26.1	●	✓	✓	✓	✓	✓	CMP-ab	EGF Lectin_C Sushi V-set Xlink	00000	10
POLG	15q26.1	●					✓	CPS-s	Metabolic pathways	0000	1
MEF2A	15q26.3	-									
<i>GRIN2A</i>	16p13.2	●●●				✓		CMP-ab	ANF_receptor Lig_chan Lig_chan- Glu_bd NMDAR2_C SBP_bac_3	00000	2
<i>PMM2</i>	16p13.2	●●●					✓	CPS-s	Metabolic pathways	0000	1
<i>ABAT</i>	16p13.2	●●●					✓	CPS-s	Metabolic pathways	0000	1
<i>MMP15</i>	16q13	●●					✓	CMP-s	4314 Hemopexin PG_binding_1 Peptidase_M10	●	17
<i>CNGB1</i>	16q13	●●					✓	CPS-ab	Olfactory transduction	0000	2
<i>GOT2</i>	16q21	●●					✓	CPS-s	Metabolic pathways	0000	1
<i>CNOT1</i>	16q21	●●					✓	CPS-ab	RNA degradation	00	6
<i>GINS3</i>	16q21	●●					✓	PPI-ab	5685, 9837, 4174, 57001, 51659	000	46
<i>ADAMTS18</i>	16q23.1	●					✓	CMP-ab	ADAM_spacer1 Pep_M12B_propep Reprolysin TSP_1	00000	5
<i>MAF</i>	16q23.1	●●					✓	CMP-ab	Maf_N bZIP_Maf	00000	27
<i>GAN</i>	16q23.2	●					✓	CMP-ab	BACK BTB Kelch_1	00000	50
<i>SDR42E1</i>	16q23.3	●					✓	CMP-ab	3Beta_HSD Epimerase NAD_binding_4 Polysacc_synt_2 RmlD_sub_bind	00000	1
<i>PLCG2</i>	16q23.3	●	✓	✓	✓	✓	✓	CPS-s	Metabolic pathways	0000	1
<i>HSD17B2</i>	16q23.3	●					✓	CPS-s	Metabolic pathways	0000	1
<i>MPHOSPH6</i>	16q23.3	●●●					✓	CPS-ab	RNA degradation	00	6
<i>COX4I1</i>	16q24.1	●					✓	CPS-s	Metabolic pathways	0000	1
<i>DHX33</i>	17p13.2	●●					✓	CMP-ab	DEAD DUF1605 HA2 Helicase_C	00000	9
<i>PIK3R5</i>	17p13.1	●					✓	CPS-s	Type II diabetes mellitus	0	1
<i>NTN1</i>	17p13.1	●	✓	✓	✓	✓	✓	CPS-ab	Axon guidance	000	2
<i>STX8</i>	17p13.1	●	✓	✓	✓	✓	✓	CPS-ab	SNARE interactions in vesicular transport	0	7
<i>ARHGAP44</i>	17p12	●●	✓	✓	✓	✓	✓	PPI-ab	5879, 51155	0	97
CORO6	17q11.2	●					✓	CMP-ab	DUF1899 DUF1900 WD40	00000	6
CCL2	17q12	-									
<i>KLHL11</i>	17q21.2	●					✓	CMP-ab	BACK BTB Kelch_1	00000	50
<i>KLHL10</i>	17q21.2	●					✓	CMP-ab	BACK BTB Kelch_1 Kelch_2	00000	22
<i>ACLY</i>	17q21.2	●					✓	CPS-s	Metabolic pathways	0000	1
<i>EIF1</i>	17q21.2	●					✓	CPS-s	VEGF, Hypoxia, and Angiogenesis	0	4
<i>ARL4D</i>	17q21.31	●					✓	CMP-ab	Arf Gtr1_RagA Miro Ras SRPRB	00000	4
<i>RND2</i>	17q21.31	●					✓	CMP-ab	Arf Miro Ras	00000	30
<i>DHX8</i>	17q21.31	●					✓	CMP-ab	DEAD DUF1605 HA2 Helicase_C	00000	9
<i>AARSD1</i>	17q21.31	●					✓	CMP-ab	tRNA-synt_2c tRNA_SAD	00000	71
<i>AOC3</i>	17q21.31	●					✓	CPS-s	Metabolic pathways	0000	1
<i>AOC2</i>	17q21.31	●					✓	CPS-s	Metabolic pathways	0000	1
<i>G6PC</i>	17q21.31	●					✓	CPS-s	Metabolic pathways	0000	1
<i>BRCA1</i>	17q21.31	●					✓	CPS-ab	BRCA1-dependent Ub-ligase activity	00	6
<i>WNT9B</i>	17q21.32	●					✓	CPS-ab	Pathways in cancer	0	9

<i>WNT3</i>	17q21.32	●				✓	✓	CPS-ab	Pathways in cancer	0	9
<i>GOSR2</i>	17q21.32	●	✓	✓	✓	✓	✓	CPS-ab	SNARE interactions in vesicular transport	0	7
<i>ITGB3</i>	17q21.32	●					✓	PPI-s	948	000	14
									26227, 10228, 8666, 9568, 3320, 3326, 6950, 1936, 3187, 10963, 3857, 5286, 10652, 5870, 4967, 5708, 2904, 6804, 65263, 255738, 1857, 5707, 80227, 9482, 7419, 6632, 6229, 6160, 3192, 55342,		
<i>NSF</i>	17q21.32	●				✓	✓	PPI-ab	23344, 51493	000	27
<i>NGFR</i>	17q21.33	●					✓	CPS-s	Cytokine-cytokine receptor interaction	000	2
<i>XYLT2</i>	17q21.33	●					✓	CPS-s	Metabolic pathways	0000	1
<i>ITGA3</i>	17q21.33	●				✓	✓	CPS-ab	Pathways in cancer	0	9
<i>PHB</i>	17q21.33	●					✓	PPI-s	3667	0000	10
<i>COL1A1</i>	17q21.33	●					✓	PPI-s	948	0	20
<i>GALR2</i>	17q25.1	●●				✓	✓	CMP-ab	7TM_GPCR_Srsx 7TM_GPCR_Srv 7tm_1	00000	73
<i>GRIN2C</i>	17q25.1	●					✓	CMP-ab	ANF_receptor Lig_chan Lig_chan-Glu_bd NMDAR2_C SBP_bac_3	00000	5
<i>RECQL5</i>	17q25.1	●●					✓	CMP-ab	DEAD Helicase_C ResIII	00000	54
<i>ITGB4</i>	17q25.1	●●				✓	✓	CMP-ab	EGF_2 Integrin_B_tail Integrin_beta	00000	15
<i>GGA3</i>	17q25.1	●			✓	✓	✓	CMP-ab	GAT VHS	00000	15
<i>CASKIN2</i>	17q25.1	●●				✓	✓	CMP-ab	SAM_1 SAM_2 SH3_2	00000	37
<i>TRIM47</i>	17q25.1	●●				✓	✓	CMP-ab	SPRY zf-B_box zf-C3HC4	00000	33
<i>TRIM65</i>	17q25.1	●●			✓	✓	✓	CMP-ab	SPRY zf-B_box zf-C3HC4	00000	10
<i>GALK1</i>	17q25.1	●●				✓	✓	CPS-s	Metabolic pathways	0000	1
<i>ACOX1</i>	17q25.1	●●	✓	✓	✓	✓	✓	CPS-s	Metabolic pathways	0000	1
<i>NT5C</i>	17q25.1	●				✓	✓	CPS-s	Metabolic pathways	0000	1
<i>SPHK1</i>	17q25.1	●●					✓	CPS-s	Metabolic pathways	0000	1
<i>AANAT</i>	17q25.1	●					✓	CPS-s	Metabolic pathways	0000	1
<i>ATP5H</i>	17q25.1	●					✓	CPS-s	Metabolic pathways	0000	1
<i>H3F3B</i>	17q25.1	●●				✓	✓	CPS-ab	Systemic lupus erythematosus	00	3
<i>GRB2</i>	17q25.1	●		✓	✓	✓	✓	PPI-s	3667	0000	1
									10845, 7428, 5428, 7327, 5300, 2632, 23395, 54995	0	172
<i>ICT1</i>	17q25.1	●					✓	PPI-ab	Insulin signaling pathway	0	1
<i>RPTOR</i>	17q25.3	●	✓	✓	✓	✓	✓	CPS-s	Insulin signaling pathway	0	1
<i>BAIAP2</i>	17q25.3	●					✓	PPI-ab	575, 8825, 5879, 55740, 23189, 8936	00	36
<i>LPIN2</i>	18p11.31	●	✓	✓	✓	✓	✓	CMP-ab	LNS2 Lipin_N	00000	68
<i>LAMA1</i>	18p11.31	●				✓	✓	CPS-ab	Pathways in cancer	000	2
<i>PTPRM</i>	18p11.23	●	✓	✓	✓	✓	✓	CPS-ab	Adherens junction	000	1
<i>HRH4</i>	18q11.2	●				✓	✓	CMP-s	1524 7TM_GPCR_Srsx 7tm_1	●	7
<i>SNRPD1</i>	18q11.2	●					✓	CPS-ab	Systemic lupus erythematosus	000	3
<i>GATA6</i>	18q11.2	●			✓	✓	✓	MIR-ab	MI0000270	00	1
<i>DSC2</i>	18q12.1	●					✓	CMP-ab	Cadherin Cadherin_C Cadherin_pro	00000	44
<i>DSC1</i>	18q12.1	●					✓	CMP-ab	Cadherin Cadherin_C Cadherin_pro	00000	44
<i>DSC3</i>	18q12.1	●	✓	✓			✓	CMP-ab	Cadherin Cadherin_C Cadherin_pro	00000	16
<i>CDH2</i>	18q12.1	●			✓			PPI-ab	2898, 2904, 165904, 1501, 5793	00	6
<i>FECH</i>	18q21.31	●			✓		✓	CPS-s	Metabolic pathways	0000	1
<i>NETO1</i>	18q22.3	●	✓	✓	✓	✓	✓	CMP-s	4040 Ldl_recept_a	●	4
<i>KCNG2</i>	18q23	●					✓	CMP-ab	Ion_trans Ion_trans_2 K_tetra	00000	56
<i>TMPRSS9</i>	19p13.3	●				✓	✓	CMP-s	4040 Ldl_recept_a	●●	4
<i>DIRAS1</i>	19p13.3	●					✓	CMP-ab	Arf Miro Ras	00000	55
<i>LINGO3</i>	19p13.3	●			✓	✓	✓	CMP-ab	I-sset V-set ig	00000	14
<i>OAZ1</i>	19p13.3	●			✓	✓	✓	CMP-ab	ODC_AZ	0000	39
<i>AMH</i>	19p13.3	●			✓	✓	✓	CPS-s	Cytokine-cytokine receptor interaction	000	2
19p13.2											
<i>RDH8</i>	19p13.2	●		✓		✓	✓	CPS-s	Metabolic pathways	0000	1
<i>DNMT1</i>	19p13.2	●				✓	✓	CPS-s	Metabolic pathways	0000	1
<i>TYK2</i>	19p13.2	●					✓	CPS-ab	Jak-STAT signaling pathway	0	10
<i>UQCRRF51</i>	19q12	●●●					✓	CPS-s	Metabolic pathways	0000	1
<i>CCNE1</i>	19q12	●●●				✓	✓	CPS-ab	Pathways in cancer	0	9
<i>CADM4</i>	19q13.31	●					✓	CMP-ab	C2-set_2 I-sset V-set ig	00000	42
									3827, 3688, 3482, 7297, 6612, 3689, 3693, 6613	00	86
<i>PLAUR</i>	19q13.31	●					✓	PPI-ab	3693, 6613	00	86
<i>BMP2</i>	20p12.3	●●	✓	✓			✓	CPS-s	Cytokine-cytokine receptor interaction	000	2
<i>CRLS1</i>	20p12.3	●●					✓	CPS-s	Metabolic pathways	0000	1
<i>JAG1</i>	20p12.2	●				✓	✓	CMP-ab	EGF EGF_2 EGF_CA	00000	58
									7TM_GPCR_Srsx 7TM_GPCR_Srv 7TM_GPCR_Srx 7tm_1	00000	28
<i>SSTR4</i>	20p11.21	●					✓	CMP-ab	Insulin signaling pathway	0	1
<i>PYGB</i>	20p11.21	●●	✓	✓	✓	✓	✓	CPS-s	Metabolic pathways	0000	1
<i>ACSS1</i>	20p11.21	●●				✓	✓	CPS-s	Metabolic pathways	0000	1
<i>NANP</i>	20p11.21	●●					✓	CPS-s	Metabolic pathways	0000	1
<i>EPB41L1</i>	20q11.23	●				✓	✓	CMP-ab	4_1_CTD FA FERM_C FERM_M	00000	1

										FERM_N SAB			
<i>MAFB</i>	20q12	●							✓	CMP-ab	Maf_N bZIP_Maf	ooooo	27
<i>KCNB1</i>	20q13.13	●							✓	CMP-ab	Ion_trans Ion_trans_2 K_tetra	ooooo	56
<i>KCNG1</i>	20q13.13	●							✓	CMP-ab	Ion_trans Ion_trans_2 K_tetra	ooooo	56
<i>DPM1</i>	20q13.13	●							✓	CPS-s	Metabolic pathways	◇◇◇◇	1
<i>ARFGEF2</i>	20q13.13	●			✓	✓	✓	✓	✓	CPS-ab	ADP-sRibosylation Factor	◇◇◇	3
<i>NFATC2</i>	20q13.2	●		✓	✓	✓	✓	✓	✓	CPS-ab	Axon guidance	◇◇◇	2
<i>NPBWR2</i>	20q13.33	●							✓	CMP-ab	7TM_GPCR_Srsx 7TM_GPCR_Srv 7tm_1	ooooo	26
<i>OPRL1</i>	20q13.33	●		✓	✓	✓	✓	✓	✓	CMP-ab	7TM_GPCR_Srx 7tm_1	ooooo	3
<i>ARFRP1</i>	20q13.33	●							✓	CMP-ab	Arf Gtr1_RagA Miro Ras SRPRB	ooooo	12
<i>CDH4</i>	20q13.33	●●							✓	CMP-ab	Cadherin Cadherin_C Cadherin_pro	ooooo	44
<i>TNFRSF6B</i>	20q13.33	●							✓	CPS-s	Cytokine-cytokine receptor interaction	◇◇◇	2
<i>UCKL1</i>	20q13.33	●							✓	CPS-s	Metabolic pathways	◇◇◇◇	1
<i>CBR3</i>	21q22.12	●							✓	CPS-s	Metabolic pathways	◇◇◇◇	1
<i>SIM2</i>	21q22.13	●●			✓	✓			✓	CMP-ab	HLH PAS PAS_3	ooooo	25
<i>HLCS</i>	21q22.13	●●							✓	CPS-s	Metabolic pathways	◇◇◇◇	1
<i>PIGP</i>	21q22.13	●●							✓	CPS-s	Metabolic pathways	◇◇◇◇	1
<i>ADARB1</i>	21q22.3	●●		✓	✓	✓	✓	✓	✓	CMP-ab	A_deamin dsrm	ooooo	4
<i>ITGB2</i>	21q22.3	●●							✓	CPS-s	Phagosome	◇	3
<i>COMT</i>	22q11.21	●							✓	CPS-s	Metabolic pathways	◇◇◇◇	1
<i>RANBP1</i>	22q11.21	●							✓	PPI-ab	23043, 7189	◇	140
<i>LRP5L</i>	22q11.23	●●●							✓	CMP-s	4040 Ldl_recept_b	●●●	2
<i>SEZ6L</i>	22q12.1	●●●		✓	✓	✓	✓	✓	✓	CMP-ab	CUB Sushi	ooooo	1
<i>TMPRSS6</i>	22q12.3	●							✓	CMP-s	4040 Ldl_recept_a	●	12
<i>RASD2</i>	22q12.3	●							✓	CMP-ab	Arf GTP_EFTU Miro Ras	ooooo	30
<i>TOM1</i>	22q12.3	●							✓	CMP-ab	GAT VHS	ooooo	15
<i>CSF2RB</i>	22q12.3	●							✓	CPS-s	Cytokine-cytokine receptor interaction	◇◇◇	2
<i>IL2RB</i>	22q12.3	●							✓	CPS-s	Cytokine-cytokine receptor interaction	◇◇◇	2
<i>MPST</i>	22q12.3	●							✓	CPS-s	Metabolic pathways	◇◇◇◇	1
<i>TST</i>	22q12.3	●							✓	CPS-s	Metabolic pathways	◇◇◇◇	1
<i>SSTR3</i>	22q13.1	●		✓	✓	✓	✓	✓	✓	CMP-ab	7TM_GPCR_Srsx 7TM_GPCR_Srv 7TM_GPCR_Srx 7tm_1	ooooo	3

Genes in previously associated loci are shaded in orange. Genes and loci in bold have been previously associated with the disease. Genes underlined are the WTCCC candidates. Key to genetic support column: HS ●●●●, MHS-●●●, MWS-●●, WS-●, no support -. Method: ab- *ab initio*, s- *seeded*. Common biological support column depends on method. For CMP-s-s-s, common gene and common domain are listed. For CMP-s-ab, only the common domain. For CPS-s-s, the common pathway is listed. For PPI-s-s, the Entrez gene ID of the gene(s) are listed. For MIR-s-s, the common miRNA ID is listed. For CRT, the common oRegAnno ID is listed. *Gentrepid* scoring: CMP-s-ab: ○○○○- $\log \chi^2 \geq 2.5$, ○○○○- $2 \leq \log \chi^2 < 2.5$, ○○○- $1.5 \leq \log \chi^2 < 2$, ○○- $1 \leq \log \chi^2 < 1.5$, ○- $\log \chi^2 < 1$. CMP-s-s-s: ●●●● - $Sc > 0.7$, ●●● - $Sc > 0.6$, ●● - $Sc > 0.5$, ●- $Sc > 0.4$. Other: ◇◇◇◇- $p < 0.005$, ◇◇◇ - $p < 0.01$, ◇◇ - $p < 0.025$, ◇- $p < 0.05$. Rank represents ranking score in prioritization of gene in specific set and search space and module, not overall ranking.

Supp. Table S2. Significantly enriched pathways for the CAD phenotype

Pathway	Resident		Nearest		Adjacent		0.1Mbp		0.5Mbp		1Mbp							
	<i>n</i>	<i>p</i>	<i>r</i>															
HS																		
<i>Ab initio</i>																		
Melanoma	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0063	1	
MHS																		
<i>Ab initio</i>																		
Steps in the Glycosylation of Mammalian N-linked Oligosaccharides	-	-	-	-	-	-	2	0.0003	1	-	-	-	2	0.0005	1	2	0.0024	1
Pathways in cancer	-	-	-	-	-	-	2	0.1076	2	-	-	-	3	0.0391	7	4	0.0734	7
Cyclins and Cell Cycle Regulation	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0013	2	2	0.0056	2
Cell Cycle: G1/S Check Point	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0019	3	2	0.0082	3
p53 signalling pathway	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0110	4	2	0.0438	4
Small cell lung cancer	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0169	5	2	0.0652	6
Cell cycle	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0342	6	2	0.1239	9
Melanoma	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0461	5	
MWS																		
<i>Seeded</i>																		
Insulin signalling pathway	2	0.0192	1	4	0.0003	1	4	0.0177	3	2	0.1473	2	4	0.3014	8	5	0.6130	20
PPAR signalling pathway	1	0.1074	3	1	0.1567	13	2	0.0947	7	2	0.0473	1	3	0.1221	2	4	0.1685	3
Aldosterone-regulated sodium reabsorption	-	-	-	2	0.0043	2	2	0.0374	4	-	-	-	1	0.5179	13	2	0.3661	10
Type II diabetes mellitus	-	-	-	2	0.0056	3	3	0.0050	1	-	-	-	1	0.5658	16	3	0.1779	4
Adipocytokine signalling pathway	-	-	-	2	0.0114	4	3	0.0137	2	-	-	-	2	0.3327	9	5	0.0577	2
IL 4 signalling pathway	-	-	-	1	0.0259	5	1	0.0776	6	-	-	-	-	-	-	1	0.2878	7
Neurotrophin signalling pathway	-	-	-	2	0.0358	6	2	0.2376	14	1	0.4694	4	2	1.0000	21	4	0.7948	25
Insulin Signalling Pathway	-	-	-	1	0.0490	7	1	0.1430	10	-	-	-	-	-	-	1	0.4772	14
IGF-1 Signalling Pathway	-	-	-	1	0.0490	7	1	0.1430	10	-	-	-	-	-	-	1	0.4772	14
<i>Ab initio</i>																		
Axon guidance	2	0.0169	1	2	0.0368	6	2	0.2430	21	2	0.1322	4	3	0.4869	26	4	0.7978	73
Insulin signalling pathway	2	0.0192	2	4	0.0003	1	4	0.0177	8	2	0.1473	5	4	0.3014	17	5	0.6130	54
Aldosterone-regulated sodium reabsorption	-	-	-	2	0.0043	2	2	0.0374	11	-	-	-	-	-	-	2	0.3661	41
Type II diabetes mellitus	-	-	-	2	0.0056	3	3	0.0050	2	-	-	-	-	-	-	3	0.1779	27
Adipocytokine signalling pathway	-	-	-	2	0.0114	4	3	0.0137	5	-	-	-	2	0.3327	19	5	0.0577	11
Neurotrophin signalling pathway	-	-	-	2	0.0358	5	2	0.2376	20	-	-	-	2	1.0000	39	4	0.7948	72
Angiotensin-converting enzyme 2 regulates heart function	-	-	-	-	-	-	2	0.0039	1	-	-	-	-	-	-	2	0.0574	10
Steps in the Glycosylation of Mammalian N-linked Oligosaccharides	-	-	-	-	-	-	2	0.0052	3	-	-	-	2	0.0265	1	2	0.0743	15
Basal cell carcinoma	-	-	-	-	-	-	3	0.0074	4	-	-	-	-	-	-	3	0.2330	32
RNA degradation	-	-	-	-	-	-	3	0.0148	6	-	-	-	2	0.3453	21	4	0.1685	25
Cell Cycle: G1/S Check Point	-	-	-	-	-	-	2	0.0175	7	-	-	-	2	0.0827	4	4	0.0095	4
Small cell lung cancer	-	-	-	-	-	-	3	0.0238	9	-	-	-	2	0.6580	30	5	0.1869	29
Pathways in cancer	-	-	-	-	-	-	6	0.0297	10	-	-	-	5	1.0000	39	11	0.6207	55
N-Glycan biosynthesis	-	-	-	-	-	-	2	0.0495	12	-	-	-	2	0.2053	13	2	0.6606	57
PPAR signalling pathway	-	-	-	-	-	-	2	0.0947	14	2	0.0473	3	3	0.1221	5	4	0.1685	25

Pathway	Resident		Nearest		Adjacent		0.1Mbp		0.5Mbp		1Mbp							
	<i>n</i>	<i>p</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>												
One carbon pool by folate	-	-	-	-	-	-	-	-	-	2	0.0034	1	2	0.0374	2	2	0.1021	19
Aminoacyl-tRNA biosynthesis	-	-	-	-	-	-	-	-	-	2	0.0171	2	2	0.1559	8	3	0.1272	21
Cyclins and Cell Cycle Regulation	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0585	3	3	0.0312	7
Amino sugar and nucleotide sugar metabolism	-	-	-	-	-	-	-	-	-	-	-	-	2	0.1990	12	5	0.0146	5
Olfactory transduction	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0010	1
E2F1 Destruction Pathway	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	0.0028	2
Regulation of p27 Phosphorylation during Cell Cycle Progression	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	0.0063	3
Cyclin E Destruction Pathway	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0287	6
WS																		
<i>Seeded</i>																		
ECM-receptor interaction	3	0.0470	1	3	0.1216	4	6	0.1387	6	4	0.1443	3	9	0.2979	12	15	0.3485	11
Insulin signalling pathway	3	0.1441	5	5	0.0471	1	8	0.2514	13	4	0.5723	14	10	1.0000	29	18	0.8052	31
Type II diabetes mellitus	-	-	-	2	0.1500	7	5	0.0339	1	1	1.0000	22	7	0.0903	5	13	0.0196	4
Insulin Signalling Pathway	-	-	-	1	0.2615	11	3	0.0430	2	1	0.3981	8	1	1.0000	29	4	0.5271	19
IGF-1 Signalling Pathway	-	-	-	1	0.2615	11	3	0.0430	2	1	0.3981	8	1	1.0000	29	4	0.5271	19
Metabolic pathways	14	0.3075	8	17	0.7819	20	36	0.3003	16	24	0.5912	16	55	0.0001	1	100	0.0000	1
Cytokine-cytokine receptor interaction	1	0.5213	9	4	0.7983	21	7	0.3326	17	3	0.2201	4	16	0.2950	11	24	0.0061	2
Hypoxia-Inducible Factor in the Cardiovascular System	-	-	-	-	-	-	1	0.4396	19	-	-	-	4	0.0227	2	6	0.0129	3
Phagosome	1	1.0000	13	2	1.0000	22	6	0.8275	29	2	0.5872	15	5	0.0424	3	15	0.1551	8
VEGF, Hypoxia, and Angiogenesis	-	-	-	-	-	-	1	1.0000	30	-	-	-	5	0.0494	4	7	0.0937	6
<i>Ab initio</i>																		
Adherens junction	4	0.0047	1	4	0.0193	3	7	0.0185	9	5	0.0281	4	9	0.1157	29	11	0.7356	172
Axon guidance	5	0.0074	2	7	0.0024	1	9	0.0616	22	8	0.0116	2	16	0.0432	15	22	0.3713	95
Vibrio cholerae infection	3	0.0145	3	3	0.0416	6	3	0.4586	102	3	0.1373	23	5	0.6022	108	7	1.0000	215
Arrhythmogenic right ventricular cardiomyopathy (ARVC)	3	0.0331	4	3	0.0890	11	5	0.2041	61	3	0.2587	38	6	0.8241	156	12	0.6148	148
Pathways in cancer	7	0.0338	5	9	0.0500	8	24	0.0014	2	11	0.2576	37	35	0.0310	9	54	0.2205	63
Protein digestion and absorption	3	0.0404	6	3	0.1062	15	5	0.2297	68	4	0.1231	22	10	0.1305	33	16	0.1456	40
SNARE interactions in vesicular transport	2	0.0458	7	2	0.0933	12	3	0.1539	50	2	0.2115	32	3	0.7515	141	7	0.3403	84
ECM-receptor interaction	3	0.0470	8	3	0.1216	18	6	0.1387	41	4	0.1443	26	9	0.2979	61	15	0.3485	86
Platelet Amyloid Precursor Protein Pathway	-	-	-	2	0.0165	2	3	0.0143	8	2	0.0426	7	2	0.2876	59	4	0.1260	36
Acute Myocardial Infarction	-	-	-	2	0.0325	4	3	0.0379	14	2	0.0811	14	2	0.6607	122	5	0.1902	54
Eicosanoid Metabolism	-	-	-	2	0.0388	5	2	0.2015	60	2	0.0957	17	2	0.6813	126	5	0.2277	66
Insulin signalling pathway	3	0.1441	17	5	0.0471	7	8	0.2514	72	4	0.5723	58	10	1.0000	164	18	0.8052	190
TGF-beta signalling pathway	-	-	-	3	0.1184	16	7	0.0390	16	4	0.1400	24	7	0.6813	125	11	0.8757	208
Type II diabetes mellitus	-	-	-	2	0.1500	22	5	0.0339	12	-	-	-	7	0.0903	23	13	0.0196	9
Olfactory transduction	2	0.5850	40	2	0.1781	25	4	0.0014	1	3	0.0360	5	6	8.70E-08	1	8	6.17E-17	2
ADP-Ribosylation Factor	-	-	-	-	-	-	4	0.0032	3	3	0.0071	1	4	0.0352	11	4	0.2877	74
Small cell lung cancer	2	0.1942	24	2	0.3442	43	9	0.0046	4	3	0.4574	56	11	0.0934	25	16	0.2121	60
Rac 1 cell motility signalling pathway	-	-	-	-	-	-	4	0.0072	5	-	-	-	5	0.0181	5	6	0.1062	31
Angiotensin-converting enzyme 2 regulates heart function	-	-	-	-	-	-	3	0.0115	6	-	-	-	2	0.2585	54	2	0.7064	166

Pathway	Resident		Nearest		Adjacent		0.1Mbp		0.5Mbp		1Mbp							
	<i>n</i>	<i>p</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>			
How does salmonella hijack a cell	-	-	-	-	-	-	2	0.0132	7	-	-	-	2	0.0492	16	2	0.1504	42
Acute myeloid leukaemia	-	-	-	2	0.1960	29	6	0.0199	10	2	0.3960	51	8	0.0749	21	13	0.0827	23
Chaperones modulate interferon Signalling Pathway	-	-	-	-	-	-	3	0.0287	11	2	0.0673	9	3	0.1516	37	4	0.3097	78
Role of PI3K subunit p85 in regulation of Actin Organization and Cell Migration	-	-	-	-	-	-	2	0.0343	13	-	-	-	-	-	2	0.3178	81	
fMLP induced chemokine gene expression in HMC-1 cells	-	-	-	-	-	-	4	0.0381	15	2	0.1940	30	3	0.7409	140	4	1.0000	215
Endometrial cancer	-	-	-	-	-	-	5	0.0425	17	2	0.3444	45	6	0.2788	56	8	0.6896	164
Insulin Signalling Pathway	-	-	-	-	-	-	3	0.0430	18	-	-	-	-	-	4	0.5271	127	
IGF-1 Signalling Pathway	-	-	-	-	-	-	3	0.0430	18	-	-	-	-	-	4	0.5271	127	
Bacterial invasion of epithelial cells	-	-	-	-	-	-	6	0.0454	19	2	0.6806	66	5	1.0000	164	7	0.3897	100
Valine, leucine and isoleucine biosynthesis	-	-	-	-	-	-	-	-	2	0.0270	3	2	0.2008	43	2	0.6623	158	
Non-small cell lung cancer	2	0.0934	12	2	0.1804	26	4	0.1465	44	4	0.0391	6	6	0.2992	62	8	0.8453	199
Metabolic pathways	14	0.3075	30	17	0.7819	62	36	0.3003	81	24	0.5912	61	55	0.0001	2	100	4.39E-09	1
Systemic lupus erythematosus	-	-	-	-	-	-	3	0.4907	106	-	-	-	3	0.0126	3	7	0.0015	3
Toxoplasmosis	-	-	-	-	-	-	3	0.4897	105	-	-	-	3	0.0177	4	12	0.1262	38
BRCA1-dependent Ub-ligase activity	-	-	-	-	-	-	-	-	-	-	-	-	3	0.0182	6	3	0.0922	26
Hypoxia-Inducible Factor in the Cardiovascular System	-	-	-	-	-	-	-	-	-	-	-	-	4	0.0227	7	6	0.0129	8
CD40L Signalling Pathway	-	-	-	-	-	-	2	0.1084	34	-	-	-	4	0.0227	7	4	0.2535	69
Tuberculosis	-	-	-	-	-	-	-	-	-	-	-	-	6	0.0300	8	13	0.0061	5
Ahr Signal Transduction Pathway	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0311	10	2	0.0994	28
Pancreatic cancer	2	0.1401	16	2	0.2594	34	5	0.1879	58	4	0.0817	15	10	0.0381	12	12	0.4860	123
Renal cell carcinoma	-	-	-	-	-	-	3	0.7481	118	-	-	-	10	0.0409	13	14	0.1678	51
Phagosome	-	-	-	2	1.0000	65	6	0.8275	126	2	0.5872	59	5	0.0424	14	15	0.1551	46
Signal Dependent Regulation of Myogenesis by Corepressor MITR	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0492	16	2	0.1504	42
VEGF, Hypoxia, and Angiogenesis	-	-	-	-	-	-	-	-	-	-	-	-	5	0.0494	17	7	0.0937	27
Cytokine-cytokine receptor interaction	-	-	-	4	0.7983	64	7	0.3326	83	3	0.2201	33	16	0.2950	60	24	0.0061	4
Retinol metabolism	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0063	6	
Drug metabolism - cytochrome P450	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	0.0103	7	
Jak-STAT signalling pathway	-	-	-	-	-	-	3	0.2875	78	-	-	-	8	0.2849	57	13	0.0355	10
Metabolism of xenobiotics by cytochrome P450	-	-	-	-	-	-	-	-	-	2	0.6869	67	2	0.1725	41	4	0.0386	11
Glutathione metabolism	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0394	12	
Arachidonic acid metabolism	-	-	-	-	-	-	-	-	-	-	-	-	-	-	3	0.0395	13	
Regulation of eIF2	-	-	-	-	-	-	-	-	-	-	-	-	2	0.1725	40	4	0.0418	14

Pathways in bold are those ranked first in the set and mapping. *n* – number of genes in search space that are in the pathway. *p* – the *p*-value showing the statistical significance of the pathway as calculated by the Fishers-test. *r* – rank of pathway based on *p*-value. *p*-values in bold are those that are significant.

Supp. Table S3. CAD CMP seeded results

Gene	Seed	Score	Domain	Resident		Near				Adjacent				0.1Mbp		0.5Mbp				1Mbp						
				WS		MWS		WS		MHS		MWS		WS		WS		MWS		WS		MWS		WS		
				<i>n</i>	<i>m</i>																					
<i>PLG</i>	<i>LPA</i>	0.826	DUF1986 Kringle Trypsin																			1	1			
<i>IRS2</i>	<i>IRS1</i>	0.753	IRS PH			1	1	1	1			1	1	1	1			1	1	1	1	1	1	1		
<i>LRP5L</i>	<i>LRP6</i>	0.675	Ldl_recept_b							1	1	1	1	2	1											
<i>NID2</i>	<i>LRP6</i>	0.66	Ldl_recept_b											1	1					1	1		1	1		
<i>NID1</i>	<i>LRP6</i>	0.599	Ldl_recept_b																1	1		1	1			
<i>SPINT1</i>	<i>LRP6</i>	0.585	Ldl_recept_a																				1	1		
<i>LDLRAD3</i>	<i>LRP6</i>	0.581	Ldl_recept_a																				1	1		
<i>TMPRSS9</i>	<i>LRP6</i>	0.532	Ldl_recept_a																	1	1		1	1		
<i>LRP11</i>	<i>LRP6</i>	0.511	Ldl_recept_a	1	1			1	1				1	1	1	1					1	1	1	1		
<i>CCR8</i>	<i>CX3CR1</i>	0.487	7TM_GPCR_Srsx 7tm_1														3	1	8	2		3	1	8	2	
<i>CCR2</i>	<i>CX3CR1</i>	0.486	7TM_GPCR_Srsx 7tm_1																				2	1		
<i>CCR5</i>	<i>CX3CR1</i>	0.486	7TM_GPCR_Srsx 7tm_1																				2	1		
<i>HRH4</i>	<i>CX3CR1</i>	0.484	7TM_GPCR_Srsx 7tm_1																				2	1		
<i>ABCA12</i>	<i>ABCA1</i>	0.479	ABC_tran	1	1			1	1				1	1	1	1					1	1	1	1		
<i>CCR1</i>	<i>CX3CR1</i>	0.474	7TM_GPCR_Srsx 7tm_1																		2	1		2	1	
<i>NETO1</i>	<i>LRP6</i>	0.469	Ldl_recept_a					1	1				1	1	1	1					1	1		1	1	
<i>CCR3</i>	<i>CX3CR1</i>	0.459	7TM_GPCR_Srsx 7tm_1										2	1							2	1		2	1	
<i>TMPRSS6</i>	<i>LRP6</i>	0.458	Ldl_recept_a																		1	1		1	1	
<i>MMP15</i>	<i>MMP3</i>	0.456	Hemopexin PG_binding_1 Peptidase_M10																				1	1	1	1
<i>LCTL</i>	<i>KL</i>	0.413	Glyco_hydro_1										2	1												

Domains have Pfam abbreviations. *n* – number of SNPs. *m* – number of clusters formed by SNPs.

Supp. Table S4. CAD CMP *ab initio* results

	Domains	<i>n</i>	Genes	χ^2_{\min}	$\chi^2_{\max \text{ unique}}$
MHS					
Resident					
	CUB Sushi	2	<i>CSMD2, SEZ6L</i>	514.2362	381046.4
	CH	2	<i>MICAL2, PARVA</i>	339.679	339.679
Nearest					
	CUB Sushi	2	<i>CSMD2, SEZ6L</i>	292.1441	217739.1
	CH	2	<i>MICAL2, PARVA</i>	192.4017	192.4017
0.1Mbp					
	CUB Sushi	2	<i>CSMD2, SEZ6L</i>	235.1991	175865.4
	CH	2	<i>MICAL2, PARVA</i>	154.6409	154.6409
0.5Mbp					
	I-set V-set ig	2	<i>KALRN, MFAP3L</i>	11.39225	411152.3
MWS					
Resident					
	CUB Sushi	2	<i>CSMD2, SEZ6L</i>	155.48	117242.3
	Sema	2	<i>PLXNA2, SEMA3C</i>	267.5191	267.5191
	CH	2	<i>MICAL2, PARVA</i>	101.7816	101.7816
Nearest					
	Sema	2	<i>PLXNA2, SEMA3C</i>	125.1611	125.1611
0.1Mbp					
	Arf Miro Ras	2	<i>RAB6A, RASL12</i>	12.09576	1136041
0.5Mbp					
	EGF_2 Integrin_B_tail Integrin_beta	2	<i>ITGB2, ITGB4</i>	98.26503	6.84E+08
	Calpain_III Peptidase_C2	2	<i>CAPN11, CAPN2, CAPN8</i>	48.95111	170562
	Proteasome Proteasome_A_N	2	<i>PSMA4, PSMA5</i>	72.72159	159724
1Mbp					
	EGF_2 Integrin_B_tail Integrin_b_cyt Integrin_beta	2	<i>ITGB2, ITGB5</i>	58.91449	2.8E+12
	EGF_2 Integrin_B_tail Integrin_beta	3	<i>ITGB2, ITGB4, ITGB5</i>	116.6326	8.2E+08
	Hemopepxin PG_binding_1 Peptidase_M10	2	<i>MMP15, MMP19</i>	21.68982	1.82E+08
	7tm_2 DUF3497 GPS	2	<i>BAIL, CELSR2</i>	36.95096	34129528
	Calpain_III Peptidase_C2	3	<i>CAPN2, CAPN9, CAPN11, CAPN8</i>	57.53464	204486.5
WS					
Resident					
	ADAM_spacer1 Pep_M12B_propep Reprolysin TSP_1	2	<i>ADAMTS2, ADAMTS7</i>	98.23837	1.33E+11
	FERM_C FERM_M FERM_N	2	<i>FARP1, FRMD4A</i>	51.20635	51478796
	EGF Laminin_G_1 Laminin_G_2	2	<i>CELSR2, EYS</i>	49.79457	34242798
	A_deamin dsrm	2	<i>ADARB1, ADARB2</i>	186.4832	272084.9
	ADAM_spacer1 TSP_1	3	<i>ADAMTS2, THSD4, ADAMTS7</i>	223.9874	221098.1
	Ded_cyto	2	<i>DOCK4, DOCK8</i>	205.5275	205.5275
	Peptidase_M1	2	<i>RNPEPL1, ERAP2</i>	151.2172	151.2172
	CH	5	<i>MICAL2, IQGAP2, PARVA, SYNE1, LIMCH1</i>	128.0159	128.0159
	Sema	3	<i>PLXNA2, SEMA3C, SEMA6D</i>	121.4744	121.4744
Nearest					
	FA FERM_C FERM_M FERM_N	2	<i>EPB41, FARP1</i>	46.49508	6.19E+10
	ADAM_spacer1 Pep_M12B_propep Reprolysin TSP_1	2	<i>ADAMTS2, ADAMTS7</i>	42.81239	6.08E+10
	7TM_GPCR_Srsx 7TM_GPCR_Srv 7TM_GPCR_Srx 7tm_1	2	<i>OPRL1, SSTR3</i>	30.32761	5.45E+08
	7tm_2 DUF3497 GPS	2	<i>BAIL, CELSR2</i>	91.83167	80024987
	FERM_C FERM_M FERM_N	3	<i>EPB41, FRMD4A, FARP1</i>	50.87639	52957708
	EGF Laminin_G_1 Laminin_G_2	2	<i>CELSR2, EYS</i>	20.72437	15656240
	7TM_GPCR_Srsx 7TM_GPCR_Srx 7tm_1	3	<i>EDNRB, SSTR3, OPRL1</i>	31.72312	687200.8
	A_deamin dsrm	2	<i>ADARB1, ADARB2</i>	83.12767	124398.5
	ADAM_spacer1 TSP_1	3	<i>ADAMTS2, THSD4, ADAMTS7</i>	99.22088	101085.6
	Fasciclin	2	<i>TGFBI, POSTN</i>	187.6007	187.6007
	TSP_1	5	<i>BAIL, ADAMTS2, RSPO3, ADAMTS7, THSD4</i>	105.3492	105.3492
Adjacent					
	3Beta_HSD Epimerase NAD_binding_4 Polysacc_synt_2 RmlD_sub_bind	2	<i>HSD3B1, SDR42E1</i>	23.77582	3.55E+15
	ANF_receptor Lig_chan Lig_chan-Glu_bd NMDAR2_C SBP_bac_3	2	<i>GRIN2A, GRIN2B</i>	82.88652	1.01E+15
	ANF_receptor Lig_chan Lig_chan-Glu_bd SBP_bac_3	3	<i>GRIK2, GRIN2A, GRIN2B</i>	24.03611	1.6E+11
	ADAM_spacer1 Pep_M12B_propep Reprolysin TSP_1	3	<i>ADAMTS2, ADAMTS7, ADAMTS18</i>	27.62923	4.34E+10
	C2 PI-PLC-X PI-PLC-Y efhand_like	2	<i>PLCG2, PLCZ1</i>	13.5984	3.79E+10

Domains	n	Genes	χ^2_{\min}	$\chi^2_{\max \text{ unique}}$
FA FERM_C FERM_M FERM_N	2	<i>EPB41, FARP1</i>	12.24698	1.97E+10
7TM_GPCR_Srsx 7TM_GPCR_Srv 7TM_GPCR_Srx 7tm_1	3	<i>OPRD1, SSTR3, OPRL1</i>	18.79237	3.89E+08
C8 TIL VWD	2	<i>LOC100652946, OTOG</i>	23.77582	3.16E+08
IRF-3 MH1 MH2	2	<i>SMAD3, SMAD5</i>	17.15232	1.1E+08
ADAM_spacer1 PLAC TSP_1	2	<i>THSD4, ADAMTS18</i>	18.69186	52800639
FERM_C FERM_M FERM_N	4	<i>EPB41, FRMD4A, RDX, FARP1</i>	24.49395	29872872
7tm_2 DUF3497 GPS	2	<i>BAIL, CELSR2</i>	26.52577	25391944
Cadherin Cadherin_C Cadherin_pro	2	<i>CDH2, DSC3</i>	26.52577	25301055
Cadherin Cadherin_2 Protocadherin	2	<i>PCDH9, PCDH7</i>	18.69186	4467453
7TM_GPCR_Srsx 7TM_GPCR_Srx 7tm_1	5	<i>EDNRB, HTR1A, SSTR3, OPRL1, OPRD1</i>	23.79386	605686.9
7TM_GPCR_Srsx 7TM_GPCR_Srv 7tm_1	3	<i>NPBWR2, OPRL1, SSTR3, OPRD1</i>	18.79237	447777.1
Maf_N bZIP_Maf	2	<i>MAF, MAFB</i>	82.88652	413522
DUF3398 Ded_cyto	2	<i>DOCK8, DOCK7</i>	36.62425	202623.7
nlz1	2	<i>ZNF703, ZNF503</i>	198.6475	198.6475
0.1Mbp				
Arf Gtr1_RagA Miro Ras SRPRB	2	<i>ARL4D, ARL15</i>	8.852718	1.56E+11
FA FERM_C FERM_M FERM_N	2	<i>EPB41, FARP1</i>	26.14788	3.69E+10
ADAM_spacer1 Pep_M12B_propep Reprolysin TSP_1	2	<i>ADAMTS2, ADAMTS7</i>	23.96221	3.62E+10
7TM_GPCR_Srsx 7TM_GPCR_Srv 7TM_GPCR_Srx 7tm_1	3	<i>OPRD1, SSTR3, OPRL1</i>	40.02228	7.31E+08
C8 TIL VWD	2	<i>LOC100652946, OTOG</i>	47.92058	5.92E+08
DUF1899 DUF1900 WD40	2	<i>CORO2A, CORO6</i>	72.08963	59749344
FERM_C FERM_M FERM_N	3	<i>EPB41, FRMD4A, FARP1</i>	28.03298	31527949
EGF Laminin_G_1 Laminin_G_2	2	<i>CELSR2, EYS</i>	10.89605	9320817
DEAD Helicase_C ResIII	2	<i>DDX56, HFM1</i>	11.08245	4464254
7TM_GPCR_Srsx 7TM_GPCR_Srv 7tm_1	3	<i>NPBWR2, OPRL1, SSTR3, OPRD1</i>	40.02228	840157.6
DUF3398 Ded_cyto	2	<i>DOCK8, DOCK7</i>	72.08963	380181.1
GAT VHS	2	<i>TOM1, GGA3</i>	47.92058	185151.1
ODC_AZ	2	<i>OAZ1, OAZ3</i>	186.1136	186.1136
BNR	2	<i>RELN, SORT1</i>	186.1136	186.1136
Ded_cyto	3	<i>DOCK4, DOCK7, DOCK8</i>	122.3826	122.3826
Fasciclin	2	<i>TGFBI, POSTN</i>	110.0906	110.0906
0.5Mbp				
4_1_CTD FA FERM_C FERM_M FERM_N SAB	2	<i>EPB41, EPB41L1</i>	19.86427	4.26E+17
3Beta_HSD Epimerase NAD_binding_4 Polysacc_synt_2 RmlD_sub_bind	2	<i>HSD3B1, SDR42E1, HSD3B2</i>	11.3442	1.94E+15
EGF_CA G2F Ldl_recept_b NIDO Thyroglobulin_1	2	<i>NID1, NID2</i>	43.47533	1.63E+15
Acyl-CoA_dh_1 Acyl-CoA_dh_2 Acyl-CoA_dh_M Acyl-CoA_dh_N	2	<i>IVD, ACAD8</i>	11.3442	7.93E+11
FA FERM_C FERM_M FERM_N	3	<i>EPB41, FARP1, EPB41L1</i>	14.10048	2.41E+10
Basic HLH Myf5	2	<i>MYF5, MYOD1</i>	106.615	8.65E+08
Furin-like Pkinase Pkinase_Tyr Recep_L_domain	2	<i>ERBB3, INSR</i>	14.64684	5.87E+08
7TM_GPCR_Srsx 7TM_GPCR_Srv 7TM_GPCR_Srx 7tm_1	3	<i>OPRD1, SSTR3, OPRL1</i>	8.003931	2.12E+08
C8 TIL VWD	2	<i>LOC100652946, OTOG</i>	11.3442	1.72E+08
EGF_2 Integrin_B_tail Integrin_beta	2	<i>ITGB2, ITGB4</i>	18.29663	1.48E+08
FERM_C FERM_M FERM_N	6	<i>EPB41, FRMD4A, FRMD6, RDX, EPB41L1, FARP1</i>	28.20097	36680268
DUF1899 DUF1900 WD40	2	<i>CORO2A, CORO6</i>	18.29663	17378405
7tm_2 DUF3497 GPS	2	<i>BAIL, CELSR2</i>	12.82798	13856991
7TM_GPCR_Srsx 7TM_GPCR_Srx 7tm_1	6	<i>ADRA2C, EDNRB, CCR1, SSTR3, OPRL1, OPRD1</i>	15.34863	475970.4
7TM_GPCR_Srsx 7TM_GPCR_Srv 7tm_1	3	<i>NPBWR2, OPRL1, SSTR3, OPRD1</i>	8.003931	244360
Calpain_III Peptidase_C2	4	<i>CAPN2, CAPN10, CAPN9, CAPN11, CAPN8</i>	38.10643	147594.4
DUF3398 Ded_cyto	2	<i>DOCK8, DOCK7</i>	18.29663	110574.8
1Mbp				
4_1_CTD FA FERM_C FERM_M FERM_N SAB	2	<i>EPB41, EPB41L1</i>	8.662955	2.22E+17
PI3K_C2 PI3K_rbd PI3Ka PI3_PI4_kinase PX	2	<i>PIK3C2A, PIK3C2G</i>	13.50584	3.54E+15
EGF_CA G2F Ldl_recept_b NIDO Thyroglobulin_1	2	<i>NID1, NID2</i>	20.83964	8.47E+14
ANF_receptor Lig_chan Lig_chan-Glu_bd NMDAR2_C SBP_bac_3	2	<i>GRIN2B, GRIN2C</i>	20.83964	2.88E+14
C2 PI-PLC-X PI-PLC-Y PLC-beta_C efhand_like	2	<i>PLCB2, PLCB3</i>	20.83964	1.54E+14
EGF_2 Integrin_B_tail Integrin_b_cyt	4	<i>ITGB1, ITGB5, ITGB3, ITGB2</i>	45.45267	2.37E+12

Domains	<i>n</i>	Genes	χ^2_{min}	$\chi^2_{max_unique}$
Integrin_beta				
AbfB C8 TIL VWD	2	<i>OTOGL, OTOG</i>	39.27833	2.24E+12
Acyl-CoA_dh_1 Acyl-CoA_dh_2 Acyl-CoA_dh_M Acyl-CoA_dh_N	3	<i>IVD, ACAD10, ACAD8</i>	12.17631	9.29E+11
AAA AAA_2 RuvB_N Vps4_C	2	<i>KATNA1, KATNAL1</i>	11.95861	1.02E+11
C2 PI-PLC-X PI-PLC-Y ehand_like	4	<i>PLCB2, PLCG2, PLCZ1, PLCB3</i>	12.55249	4.31E+10
FA FERM_C FERM_M FERM_N	4	<i>EPB41, EPB41LAB, FARP1, EPB41LI</i>	11.06338	2.23E+10
EGF Kringle Trypsin fn1	2	<i>HGFAC, PLAT</i>	9.588936	9.28E+09
Cu_amine_oxid Cu_amine_oxidN2 Cu_amine_oxidN3	2	<i>ABP1, AOC3, AOC2</i>	24.92941	8E+09
EGF_2 Integrin_B_tail Integrin_beta	5	<i>ITGB1, ITGB4, ITGB2, ITGB3, ITGB5</i>	62.32352	4.82E+08
Basic HLH Myf5	2	<i>MYF5, MYOD1</i>	53.65041	4.51E+08
C8 TIL VWD	3	<i>LOC100652946, OTOG, OTOGL</i>	12.17631	2.02E+08
I-set Pkinase Pkinase_Tyr V-set ig	2	<i>FLT1, MYLK, KALRN</i>	9.343546	53116135
ADAM_spacer1 PLAC TSP_1	3	<i>ADAMTSL2, ADAMTSL8, THSD4</i>	9.020443	33759929
FERM_C FERM_M FERM_N	7	<i>EPB41, FRMD4A, FRMD6, RDX, PTPN3, EPB41LI, EPB41LAB, FARP1</i>	15.60326	25997574
DUF1899 DUF1900 WD40	3	<i>CORO2A, CORO6, CORO1B</i>	20.25876	20361007
Cadherin Cadherin_C Cadherin_pro	3	<i>CDH4, DSC2, DSC3, DSC1</i>	13.89668	16177109
7TM_GPCR_Srv 7TM_GPCR_Srx 7tm_1	5	<i>OPRD1, PTGFR, OPRL1, SSTR3, SSTR4</i>	10.57606	1496833
7TM_GPCR_Srsx 7TM_GPCR_Srx 7tm_1	9	<i>ADRA2C, PTGER2, EDNRB, CHRM3, CCR1, SSTR3, OPRL1, SSTR4, OPRD1</i>	15.08068	557655.8
LNS2 Lipin_N	2	<i>LPIN2, LPIN1</i>	39.27833	392593.3
7TM_GPCR_Srsx 7TM_GPCR_Srv 7tm_1	5	<i>NPBWR2, HTR2B, OPRL1, SSTR3, SSTR4, OPRD1</i>	10.57606	353453.9
tRNA-synt_2c tRNA_SAD	2	<i>AARS2, AARSD1</i>	24.92941	287900.7
RNase_PH RNase_PH_C	2	<i>EXOSC7, PNPT1</i>	13.50584	157034.9
Pkinase Pkinase_C Pkinase_Tyr	6	<i>PRKCH, LATS1, RPS6KA4, SGK1, RPS6KB2, CDC42BPB</i>	8.258661	116488.7

Domains have Pfam abbreviations. Results are filtered on threshold of $\chi^2_{max_unique} > 10^5$ and $\chi^2_{min} > 7.88$ for multidomain proteins, and $\chi^2_{min} > 100$ for single domain proteins. *n* – number of genes. Genes are those with the homologous domains.

Supp. Table S5. CAD PPI seeded interactions, with scores and ranks

	Candidate gene	Interacting gene	Resident			Nearest			Adjacent			0.1Mbp			0.5Mbp			1Mbp		
			<i>n</i>	<i>p</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>
MHS																				
	<i>LIMK1</i>	<i>ABCA1</i>	-	-	-	-	-	-	-	-	-	-	-	-	1	0.1167	1	1	0.2100	1
MWS																				
	<i>TP53BP2</i>	<i>IRS1</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	0.5876	1
	<i>HSP90AB1</i>	<i>IRS1</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	0.5876	1
	<i>LIMK1</i>	<i>ABCA1</i>	-	-	-	-	-	-	-	-	-	-	-	1	0.4929	1	1	1	2	-
	<i>AGTR1</i>	<i>NOS3</i>	-	-	-	-	-	-	1	0.1635	1	-	-	-	-	-	-	-	-	-
WS																				
	<i>ARHGEF11</i>	<i>ABCA1</i>	-	-	-	-	-	-	-	-	1	0.0156	1	1	0.2182	1	1	0.8156	7	
	<i>DLG5</i>	<i>ABCA1</i>	-	-	-	-	-	-	-	-	1	0.0156	1	1	0.2182	1	1	0.8156	7	
	<i>LIN7A</i>	<i>ABCA1</i>	-	-	-	-	-	1	0.6581	5	1	0.0156	1	1	0.2182	1	1	0.8156	7	
	<i>NFATC2</i>	<i>ABCA1</i>	1	0.3247	2	1	0.4485	3	1	0.6581	5	1	0.0156	1	1	0.2182	1	1	0.8156	7
	<i>IRS1</i>	<i>GRB2</i>	2	0.3013	1	3	0.2321	1	6	0.3108	2	3	0.7552	2	5	0.2789	2	12	0.4088	3
	<i>RPTOR</i>	<i>IRS1</i>	1	0.3013	1	1	0.2321	1	1	0.3108	2	1	0.7552	2	1	0.2789	2	1	0.4088	3
	<i>SMAD3</i>	<i>IRS1</i>	1	0.3013	1	1	0.2321	1	1	0.3108	2	1	0.7552	2	1	0.2789	2	1	0.4088	3
	<i>GRB2</i>	<i>IRS1</i>	-	-	-	-	-	-	1	0.3108	2	1	0.7552	2	1	0.2789	2	1	0.4088	3
	<i>GRIN2B</i>	<i>IRS1</i>	-	-	-	1	0.2321	1	1	0.3108	2	-	-	-	1	0.2789	2	1	0.4088	3
	<i>NOS3</i>	<i>HSP90AA1</i>	-	-	-	1	0.2959	2	3	0.0537	1	-	-	-	2	0.6936	5	3	1	8
	<i>EDNRB</i>	<i>NOS3</i>	-	-	-	1	0.2959	2	1	0.0537	1	-	-	-	1	0.6936	5	1	1	8
	<i>HSP90AA1</i>	<i>NOS3</i>	-	-	-	-	-	-	1	0.0537	1	-	-	-	1	0.6936	5	1	1	8
	<i>AGTR1</i>	<i>NOS3</i>	-	-	-	-	-	-	1	0.0537	1	-	-	-	-	-	-	-	-	-
	<i>TUB</i>	<i>IRS1</i>	-	-	-	-	-	-	1	0.3108	2	-	-	-	1	0.2789	2	1	0.4088	3
	<i>HNRNPU</i>	<i>IRS1</i>	-	-	-	-	-	-	1	0.3108	2	-	-	-	-	-	-	1	0.4088	3
	<i>TIMP3</i>	<i>MMP3</i>	-	-	-	-	-	-	1	0.5179	3	-	-	-	-	-	-	1	0.7407	6
	<i>CCR3</i>	<i>CCL2</i>	-	-	-	-	-	-	1	0.5535	4	-	-	-	1	0.6722	4	1	0.2006	1
	<i>LIMK1</i>	<i>ABCA1</i>	-	-	-	-	-	-	-	-	-	-	-	-	1	0.2182	1	1	0.8156	7
	<i>WNT3</i>	<i>KL</i>	-	-	-	-	-	-	-	-	-	-	-	-	1	0.4262	3	1	1	9
	<i>CCR1</i>	<i>CCL2</i>	-	-	-	-	-	-	-	-	-	-	-	-	1	0.6722	4	1	0.2006	1
	<i>DARC</i>	<i>CCL2</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	0.2006	1
	<i>CCR2</i>	<i>CCL2</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	0.2006	1
	<i>CCR5</i>	<i>CCL2</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	0.2006	1
	<i>FNI</i>	<i>LPA</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	0.3628	2
	<i>CANX</i>	<i>LPA</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	0.3628	2

Candidate gene	Interacting gene	Resident			Nearest			Adjacent			0.1Mbp			0.5Mbp			1Mbp		
		<i>n</i>	<i>p</i>	<i>r</i>															
<i>PHB</i>	<i>IRS1</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	0.4088	3
<i>JAK2</i>	<i>IRS1</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	0.4088	3
<i>TP53BP2</i>	<i>IRS1</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	0.4088	3
<i>HSP90AB1</i>	<i>IRS1</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	0.4088	3
<i>TYK2</i>	<i>IRS1</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	0.4088	3
<i>RAD51</i>	<i>IRS1</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	0.4088	3
<i>APOA1</i>	<i>PON1</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	0.4510	4
<i>ITGB3</i>	<i>CD36</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	0.7304	5
<i>COL1A1</i>	<i>CD36</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	0.7304	5
<i>ITGB1</i>	<i>CD36</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	0.7304	5
<i>BCAN</i>	<i>MMP3</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	0.7407	6
<i>PLG</i>	<i>MMP3</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	0.7407	6
<i>ACTN2</i>	<i>NOS3</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	1	8

Abbreviations: *n* – number of genes in search space that are interacting with gene. *p* – the *p*-value showing the statistical significance of the interaction as calculated by the Fishers-test. *r* – rank of gene based on *p*-value of interaction. *P*-values in bold are those that are significant.

Supp. Table S6. CAD PPI *ab initio* significant interactions and predictions for the MHS and MWS sets

Gene	Adjacent			0.5Mbp			1Mbp		
	<i>n</i>	<i>P</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>
MHS									
<i>CLIP2</i>	-	-	-	-	-	-	1	0.0297	1
<i>CLASP1</i>	-	-	-	-	-	-	1	0.0586	2
<i>GTF2I</i>	-	-	-	-	-	-	1	0.2786	3
<i>USP7</i>	-	-	-	-	-	-	1	1	4
MWS									
<i>ELAVL2</i>	1	0.0305	1	-	-	-	-	-	-
<i>KLHDC10</i>	1	0.7254	2	2	0.3328	19	5	0.3652	28
<i>UBE2G2</i>	-	-	-	9	0.0137	1	13	0.0286	2
<i>GINS3</i>	-	-	-	2	0.0204	2	2	0.0615	6
<i>RNF157</i>	-	-	-	1	0.0342	3	1	0.0621	7
<i>MAP1LC3B</i>	-	-	-	-	-	-	2	0.0263	1
<i>ENTPD6</i>	-	-	-	-	-	-	2	0.0452	3

Abbreviations: *n* – number of genes in search space that are interacting with gene. *p* – the *p*-value showing the statistical significance of the interaction as calculated by the Fishers-test. *r* – rank of gene based on *p*-value of interaction. *P*-values in bold are those that are significant.

Supp. Table S7. CAD PPI *ab initio* interactions for the WS sets

Gene	Resident			Nearest			Adjacent			0.1Mbp			0.5Mbp			1Mbp		
	<i>n</i>	<i>p</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>
<i>JPH1</i>	1	0.0394	1	1	0.0591	3	1	0.1423	25	1	0.0959	6	1	0.2719	76	1	0.4510	197
<i>PLD1</i>	2	0.0476	2	2	0.0979	5	3	0.1436	26	2	0.2161	14	3	0.7473	171	4	0.8106	310
<i>NRP1</i>	-	-	-	2	0.0267	1	3	0.0243	3	2	0.0656	3	5	0.0073	4	6	0.0227	13
<i>SEMA3A</i>	-	-	-	1	0.0447	2	1	0.1087	22	1	0.0728	5	1	0.2118	58	1	0.3622	167
<i>SEMA3C</i>	-	-	-	1	0.0447	2	1	0.1087	22	1	0.0728	5	1	0.2118	58	1	0.3622	167
<i>PRDM4</i>	-	-	-	-	-	-	2	0.0041	1	-	-	-	2	0.0165	7	2	0.0527	31
<i>CDH2</i>	-	-	-	-	-	-	5	0.0148	2	-	-	-	-	-	-	-	-	-
<i>RPSA</i>	-	-	-	1	0.3804	15	2	0.0259	4	3	0.4959	28	11	0.2354	65	24	0.3632	169
<i>ERAP1</i>	-	-	-	-	-	-	2	0.0262	5	-	-	-	2	0.0944	31	2	0.2533	122
<i>EIF1</i>	-	-	-	-	-	-	2	0.0341	6	-	-	-	2	0.1197	36	2	0.3085	144
<i>SUPT3H</i>	-	-	-	-	-	-	4	0.0413	7	-	-	-	6	0.0468	18	7	0.3230	149
<i>MS4A2</i>	-	-	-	-	-	-	2	0.0427	8	-	-	-	2	0.1464	41	2	0.3628	168
<i>LAT2</i>	-	-	-	-	-	-	-	-	2	0.0198	1	2	0.1464	41	2	0.3628	168	
<i>MACROD1</i>	-	-	-	-	-	-	1	0.0739	15	1	0.0491	2	1	0.1467	42	1	0.2590	127
<i>TRIM14</i>	-	-	-	-	-	-	-	-	1	0.0491	2	1	0.1467	42	1	0.2590	127	
<i>GINS3</i>	-	-	-	-	-	-	1	0.3929	66	-	-	-	5	0.0020	1	5	0.0254	14
<i>VEGFA</i>	-	-	-	-	-	-	-	-	-	-	-	-	6	0.0050	2	7	0.0254	15
<i>SACM1L</i>	-	-	-	-	-	-	-	-	-	-	-	-	1	0.0070	3	8	0.0837	41
<i>DDX56</i>	-	-	-	-	-	-	2	0.1798	31	-	-	-	3	0.0094	5	13	0.1383	67
<i>UCHL1</i>	-	-	-	-	-	-	-	-	-	-	-	-	6	0.0119	6	8	0.0212	12
<i>MLH1</i>	-	-	-	-	-	-	-	-	-	-	-	-	11	0.0167	8	15	0.0513	30
<i>KPNA1</i>	-	-	-	-	-	-	-	-	-	-	-	-	7	0.0174	9	9	0.0848	42
<i>IPO5</i>	-	-	-	-	-	-	-	-	-	-	-	-	5	0.0182	10	10	0.0015	3
<i>ARNT2</i>	-	-	-	-	-	-	-	-	-	-	-	-	3	0.0185	11	3	0.0878	43
<i>BAIAP2</i>	-	-	-	-	-	-	-	-	-	-	-	-	6	0.0202	12	6	0.2817	135
<i>GPC1</i>	-	-	-	-	-	-	-	-	-	-	-	-	3	0.0262	13	4	0.0263	16
<i>LATS1</i>	-	-	-	-	-	-	-	-	-	-	-	-	3	0.0262	13	3	0.1185	56
<i>RERE</i>	-	-	-	-	-	-	-	-	-	-	-	-	5	0.0271	14	7	0.0322	19
<i>SIM2</i>	-	-	-	1	0.0591	3	1	0.1423	25	-	-	-	2	0.0314	15	2	0.0958	51
<i>ARHGAP44</i>	-	-	-	-	-	-	1	0.1423	25	-	-	-	2	0.0314	15	2	0.0958	51
<i>TRIM22</i>	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0314	15	2	0.0958	51
<i>WDR47</i>	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0314	15	2	0.0958	51
<i>POLR3A</i>	-	-	-	1	0.7268	22	2	0.1799	32	1	0.2693	19	4	0.0351	16	13	0.1391	69
<i>KALRN</i>	-	-	-	1	0.2283	9	2	0.1327	24	-	-	-	4	0.0359	17	5	0.0761	39
<i>ARC</i>	-	-	-	-	-	-	1	0.1746	30	-	-	-	2	0.0497	19	2	0.1452	75

Gene	Resident			Nearest			Adjacent			0.1Mbp			0.5Mbp			1Mbp		
	<i>n</i>	<i>p</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>									
<i>VEGFB</i>	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0497	19	4	0.0017	4
<i>CTR9</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	0.0002	1
<i>ABCF2</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0007	2
<i>NSF</i>	-	-	-	-	-	-	-	-	-	-	-	-	20	0.1849	53	32	0.0076	5
<i>WASF1</i>	-	-	-	-	-	-	2	0.3405	57	-	-	-	5	0.0926	29	10	0.0093	6
<i>ERO1LB</i>	-	-	-	-	-	-	-	-	-	2	1.0000	42	2	0.0907	28	4	0.0150	7
<i>PLG</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	14	0.0150	8
<i>PLAUR</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8	0.0167	9
<i>XPO5</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0196	10
<i>NCBP1</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	10	0.0207	11
<i>CD82</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8	0.0212	12
<i>SORT1</i>	-	-	-	-	-	-	-	-	-	-	-	-	1	1.0000	199	5	0.0254	14
<i>CDK2</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	32	0.0272	17
<i>SPATA5</i>	-	-	-	-	-	-	-	-	-	-	-	-	1	0.1258	37	2	0.0289	18
<i>ASAH1</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	1	0.0363	20
<i>FYCO1</i>	-	-	-	-	-	-	-	-	-	-	-	-	19	0.1767	51	34	0.0380	21
<i>CASC5</i>	-	-	-	-	-	-	-	-	-	-	-	-	1	0.3788	98	3	0.0388	22
<i>PRKCH</i>	-	-	-	-	-	-	1	0.5179	76	-	-	-	1	1.0000	199	6	0.0390	23
<i>TGFBI</i>	-	-	-	1	0.1414	6	2	0.0521	9	1	0.2228	15	2	0.1741	49	4	0.0391	24
<i>ING1</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	2	0.0401	25
<i>RABGAP1</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	27	0.0432	26
<i>RANBP1</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8	0.0439	27
<i>ICT1</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	8	0.0439	27
<i>CDC7</i>	-	-	-	-	-	-	1	0.7240	94	-	-	-	8	0.0682	23	13	0.0485	28
<i>TRMT112</i>	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	6	0.0493	29

Abbreviations: *n* – number of genes in search space that are interacting with gene. *p* – the *p*-value showing the statistical significance of the interaction as calculated by the Fishers-test. *r* – rank of gene based on *p*-value of interaction. *P*-values in bold are those that are significant.

Supp. Table S8. CRT and MIR results for the CAD phenotype

Regulatory element	Nearest			Adjacent			0.5Mbp			1Mbp			Candidate gene(s)
	<i>n</i>	<i>p</i>	<i>r</i>	<i>N</i>	<i>p</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>	<i>n</i>	<i>p</i>	<i>r</i>	
MWS													
Seeded mode													
hsa-mir-126	1	0.0317	1	1	0.1220	1	-	-	-	1	0.2051	1	<i>IRS1</i>
hsa-mir-145	1	0.0370	2	1	0.1412	2	-	-	-	1	0.2355	2	<i>IRS1</i>
OREG0005309	1	0.0061	1	1	0.0198	1	-	-	-	1	0.0357	1	<i>IRS1</i>
WS													
Seeded mode													
OREG0005309	1	0.0190	1	1	0.0562	1	-	-	-	1	0.1467	1	<i>IRS1</i>
Ab initio mode													
hsa-mir-181b-1	-	-	-	2	0.0552	1	3	0.0201	1	3	0.0883	2	<i>CDX2, GATA6, AIDA</i>
hsa-mir-181b-2	-	-	-	2	0.0552	1	3	0.0201	1	3	0.0883	2	<i>CDX2, GATA6, AIDA</i>
hsa-mir-148a	-	-	-	-	-	-	2	0.0244	2	2	0.0704	1	<i>TGIF2-C20orf24, DNMT1</i>
hsa-mir-181c	-	-	-	-	-	-	2	0.0244	2	2	0.0704	1	<i>CDX2, GATA6</i>
hsa-mir-181a-1	-	-	-	-	-	-	2	0.1351	3	2	0.3226	5	<i>CDX2, GATA6</i>
hsa-mir-181a-2	-	-	-	-	-	-	2	0.1351	3	2	0.3226	5	<i>CDX2, GATA6</i>

Abbreviations: *n* – number of genes in search space that are regulated by a regulatory element. *p* – the *p*-value showing the statistical significance of the regulatory element as calculated by the Fishers-test. *r* – rank of regulatory element based on *p*-value. *P*-values in bold are those that are significant.

Supp. Table S9. CARDIoGRAMplusC4D study loci and candidate genes

Chromosome	SNP	Nearest gene(s)
1	rs4845625	<i>IL6R</i>
2	rs6544713	<i>ABCG5</i>
2	rs6544713	<i>ABCG8</i>
2	rs515135	<i>APOB</i>
2	rs2252641	<i>ZEB2</i>
2	rs2252641	<i>ACVR2A</i>
2	rs1561198	<i>GGCX</i>
2	rs1561198	<i>VAMP8</i>
4	rs7692387	<i>GUCY1A3</i>
4	rs1878406	<i>EDNRA</i>
5	rs273909	<i>SLC22A4</i>
5	rs273909	<i>SLC22A5</i>
6	rs10947789	<i>KCNK5</i>
6	rs4252120	<i>PLG</i>
7	rs2023938	<i>HDAC9</i>
8	rs264	<i>LPL</i>
8	rs2954029	<i>TRIB1</i>
13	rs9319428	<i>FLT1</i>
15	rs17514846	<i>FURIN</i>
15	rs17514846	<i>FES</i>